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SEQUENCE LISTING

```
<110> Yocum, R. Rogers
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<120> METHODS AND MICROORGANISMS FOR PRODUCTION OF
      PANTO-COMPOUNDS

<130> BGI-141CP

<140> USSN 09/667,569
<141> 2000-09-21

<150> USSN 09/400,494
<151> 1999-09-21

<150> USSN 60/210,072
<151> 2000-06-07

<150> USSN 60/221,938
<151> 2000-07-28

<150> USSN 60/227,860
<151> 2000-08-24

<160> 94

<170> PatentIn Ver. 2.0

<210> 1
<211> 311
<212> PRT
<213> Haemophilus influenzae

<400> 1
Met Glu Phe Ser Thr Gln Gln Thr Pro Phe Leu Ser Phe Asn Arg Glu
  1               5                  10                  15

Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln
             20                  25                  30

Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu
         35                  40                  45

Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile
     50                  55                  60

Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg
 65                  70                  75                  80

Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala
                 85                  90                  95

Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His
            100                 105                 110

Trp Pro Thr Glu Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu
        115                 120                 125
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```
Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
    130                 135                 140

Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
145                 150                 155                 160

Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
                165                 170                 175

Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
            180                 185                 190

Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
        195                 200                 205

Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
    210                 215                 220

Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
225                 230                 235                 240

Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
                245                 250                 255

Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
            260                 265                 270

Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
        275                 280                 285

Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
    290                 295                 300

Glu Leu Ile Lys Leu Arg Lys
305                 310


<210> 2
<211> 316
<212> PRT
<213> Escherichia coli

<400> 2
Met Ser Ile Lys Glu Gln Thr Leu Met Thr Pro Tyr Leu Gln Phe Asp
 1               5                   10                  15

Arg Asn Gln Trp Ala Ala Leu Arg Asp Ser Val Pro Met Thr Leu Ser
             20                  25                  30

Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
         35                  40                  45

Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
     50                  55                  60

Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu Glu Gln Phe Leu
 65                  70                  75                  80

Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
                 85                  90                  95
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```
Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
            100                 105                 110

Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
        115                 120                 125

Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
    130                 135                 140

Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
145                 150                 155                 160

Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
                165                 170                 175

His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
            180                 185                 190

Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
        195                 200                 205

Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
    210                 215                 220

Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
225                 230                 235                 240

Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
                245                 250                 255

Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
            260                 265                 270

Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
        275                 280                 285

Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
    290                 295                 300

Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
305                 310                 315


<210> 3
<211> 319
<212> PRT
<213> Bacillus subtilis

<400> 3
Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
 1               5                  10                  15

Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
             20                  25                  30

Gln Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
         35                  40                  45

Gln Gly Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
     50                  55                  60
```

```
His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
 65                  70                  75                  80

Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
                 85                  90                  95

Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
            100                 105                 110

Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
        115                 120                 125

Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
    130                 135                 140

Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
145                 150                 155                 160

Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
                165                 170                 175

Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
            180                 185                 190

Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
        195                 200                 205

Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
    210                 215                 220

Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
225                 230                 235                 240

Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
                245                 250                 255

Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
            260                 265                 270

Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
        275                 280                 285

Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
    290                 295                 300

Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
305                 310                 315


<210> 4
<211> 312
<212> PRT
<213> Mycobacterium leprae

<400> 4
Met Pro Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Lys
  1                                  10                  15

Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
             20                  25                  30
```

```
Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
        35                  40                  45

Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
    50                  55                  60

Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
65                  70                  75                  80

Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
                85                  90                  95

Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
            100                 105                 110

Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
        115                 120                 125

Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
    130                 135                 140

His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
145                 150                 155                 160

Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
                165                 170                 175

Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
            180                 185                 190

Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
        195                 200                 205

Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
    210                 215                 220

Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
225                 230                 235                 240

Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
                245                 250                 255

Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
            260                 265                 270

Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
        275                 280                 285

Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
    290                 295                 300

Asn Arg Leu Arg Leu Arg Lys Leu
305                 310
```

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<210> [illegible]
<211> [illegible]
<212> PRT
<213> Mycobacterium tuberculosis

<400> [illegible]
```

```
Met Ser Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Arg
1               5                   10                  15

Gln Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
            20                  25                  30

Glu Leu Val Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
        35                  40                  45

Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
    50                  55                  60

Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
65                  70                  75                  80

Pro Gln Gln Asn Pro Asp Arg Pro Val Pro Phe Ile Ile Gly Val Ala
                85                  90                  95

Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
            100                 105                 110

Leu Leu Ala Arg Trp Asp His His Pro Arg Val Asp Leu Val Thr Thr
        115                 120                 125

Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gln Arg Arg Asn Leu Met
    130                 135                 140

His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
145                 150                 155                 160

Phe Val Thr Ser Val Lys Ser Gly Ser Asp Tyr Ala Cys Ala Pro Val
                165                 170                 175

Tyr Ser His Leu His Tyr Asp Ile Ile Pro Gly Ala Glu Gln Val Val
            180                 185                 190

Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
        195                 200                 205

Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
    210                 215                 220

Asp Ala Arg Ile Glu Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
225                 230                 235                 240

Ala Met Arg Thr Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
                245                 250                 255

Tyr Ala Ala Phe Ser Asp Ser Gln Ala Val Val Ala Ala Arg Glu Ile
            260                 265                 270

Trp Arg Thr Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
        275                 280                 285

Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
    290                 295                 300

Asn Arg Leu Arg Leu Arg Lys Leu
305                 310
```

```
<210> 6
<211> 329
<212> PRT
<213> Streptomyces coelicolor

<400> 6
Met Ile Ser Pro Val Pro Ser Ile Pro Arg Ser Ala His Arg Gln Arg
 1               5                  10                  15

Pro Glu Ala Thr Pro Tyr Val Asp Leu Thr Arg Pro Glu Trp Ser Ala
            20                  25                  30

Leu Arg Asp Lys Thr Pro Leu Pro Leu Thr Ala Glu Glu Val Glu Lys
        35                  40                  45

Leu Arg Gly Leu Gly Asp Val Ile Asp Leu Asp Glu Val Arg Asp Ile
    50                  55                  60

Tyr Leu Pro Leu Ser Arg Leu Leu Asn Leu Tyr Val Gly Ala Thr Asp
65                  70                  75                  80

Gly Leu Arg Gly Ala Leu Asn Thr Phe Leu Gly Glu Gln Gly Ser Gln
                85                  90                  95

Ser Gly Thr Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly
            100                 105                 110

Lys Ser Thr Val Ala Arg Leu Leu Gln Ala Leu Leu Ser Arg Trp Pro
        115                 120                 125

Glu His Pro Arg Val Glu Leu Val Thr Thr Asp Gly Phe Leu Leu Pro
    130                 135                 140

Thr Arg Glu Leu Glu Ala Arg Gly Leu Met Ser Arg Lys Gly Phe Pro
145                 150                 155                 160

Glu Ser Tyr Asp Arg Arg Ala Leu Thr Arg Phe Val Ala Asp Ile Lys
                165                 170                 175

Ala Gly Lys Ala Glu Val Thr Ala Pro Val Tyr Ser His Leu Ile Tyr
            180                 185                 190

Asp Ile Val Pro Asp Gln Arg Leu Val Val Arg Arg Pro Asp Ile Leu
        195                 200                 205

Ile Val Glu Gly Leu Asn Val Leu Gln Pro Ala Leu Pro Gly Lys Asp
    210                 215                 220

Gly Arg Thr Arg Val Gly Leu Ala Asp Tyr Phe Asp Phe Ser Val Tyr
225                 230                 235                 240

Val Asp Ala Arg Thr Glu Asp Ile Glu Arg Trp Tyr Leu Asn Arg Phe
                245                 250                 255

Arg Lys Leu Arg Ala Thr Ala Phe Gln Asn Pro Ser Ser Tyr Ile Arg
            260                 265                 270

Lys Tyr Thr Gln Val Ser Glu Glu Glu Ala Leu Arg Tyr Ala Arg Thr
        275                 280                 285

Thr Trp Arg Thr Ile Asn Lys Pro Asn Leu Val Glu Asn Val Ala Pro
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```
    290                 295                 300

Thr Arg Gly Arg Ala Thr Leu Val Leu Arg Lys Gly Pro Asp His Lys
305                 310                 315                 320

Val Gln Arg Leu Ser Leu Arg Lys Leu
                325


<210> 7
<211> 265
<212> PRT
<213> Streptomyces coelicolor

<400> 7
Met Leu Leu Thr Ile Asp Val Gly Asn Thr His Thr Val Leu Gly Leu
 1               5                   10                  15

Phe Asp Gly Glu Asp Ile Val Glu His Trp Arg Ile Ser Thr Asp Ser
             20                  25                  30

Arg Arg Thr Ala Asp Glu Leu Ala Val Leu Leu Gln Gly Leu Met Gly
         35                  40                  45

Met His Pro Leu Leu Gly Asp Glu Leu Gly Asp Gly Ile Asp Gly Ile
     50                  55                  60

Ala Ile Cys Ala Thr Val Pro Ser Val Leu His Glu Leu Arg Glu Val
 65                  70                  75                  80

Thr Arg Arg Tyr Tyr Gly Asp Val Pro Ala Val Leu Val Glu Pro Gly
                 85                  90                  95

Val Lys Thr Gly Val Pro Ile Leu Thr Asp His Pro Lys Glu Val Gly
            100                 105                 110

Ala Asp Arg Ile Ile Asn Ala Val Ala Ala Val Glu Leu Tyr Gly Gly
        115                 120                 125

Pro Ala Ile Val Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Ala Val
    130                 135                 140

Ser Ala Arg Gly Glu Tyr Ile Gly Gly Val Ile Ala Pro Gly Ile Glu
145                 150                 155                 160

Ile Ser Val Glu Ala Leu Gly Val Lys Gly Ala Gln Leu Arg Lys Ile
                165                 170                 175

Glu Val Ala Arg Pro Arg Ser Val Ile Gly Lys Asn Thr Val Glu Ala
            180                 185                 190

Met Gln Ser Gly Ile Val Tyr Gly Phe Ala Gly Gln Val Asp Gly Val
        195                 200                 205

Val Asn Arg Met Ala Arg Glu Leu Ala Asp Asp Pro Asp Asp Val Thr
    210                 215                 220

Val Ile Ala Thr Gly Gly Leu Ala Pro Met Val Leu Gly Glu Ser Ser
225                 230                 235                 240

Val Ile Asp Glu His Glu Pro Trp Leu Thr Leu Met Gly Leu Arg Leu
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            245                 250                 255

Val Tyr Glu Arg Asn Val Ser Arg Met
        260                 265


<210> 6
<211> 272
<212> PRT
<213> Mycobacterium tuberculosis

<400> 6
Met Leu Leu Ala Ile Asp Val Arg Asn Thr His Thr Val Val Gly Leu
1               5                   10                  15

Leu Ser Gly Met Lys Glu His Ala Lys Val Val Gln Gln Trp Arg Ile
            20                  25                  30

Arg Thr Glu Ser Glu Val Thr Ala Asp Glu Leu Ala Leu Thr Ile Asp
        35                  40                  45

Gly Leu Ile Gly Glu Asp Ser Glu Arg Leu Thr Gly Thr Ala Ala Leu
    50                  55                  60

Ser Thr Val Pro Ser Val Leu His Glu Val Arg Ile Met Leu Asp Gln
65                  70                  75                  80

Tyr Trp Pro Ser Val Pro His Val Leu Ile Glu Pro Gly Val Arg Thr
                85                  90                  95

Gly Ile Pro Leu Leu Val Asp Asn Pro Lys Glu Val Gly Ala Asp Arg
            100                 105                 110

Ile Val Asn Cys Leu Ala Ala Tyr Asp Arg Phe Arg Lys Ala Ala Ile
        115                 120                 125

Val Val Asp Phe Gly Ser Ser Ile Cys Val Asp Val Val Ser Ala Lys
    130                 135                 140

Gly Glu Phe Leu Gly Gly Ala Ile Ala Pro Gly Val Gln Val Ser Ser
145                 150                 155                 160

Asp Ala Ala Ala Ala Arg Ser Ala Ala Leu Arg Arg Val Glu Leu Ala
                165                 170                 175

Arg Pro Arg Ser Val Val Gly Lys Asn Thr Val Glu Cys Met Gln Ala
            180                 185                 190

Gly Ala Val Phe Gly Phe Ala Gly Leu Val Asp Gly Leu Val Gly Arg
        195                 200                 205

Ile Arg Glu Asp Val Ser Gly Phe Ser Val Asp His Asp Val Ala Ile
    210                 215                 220

Val Ala Thr Gly His Thr Ala Pro Leu Leu Leu Pro Glu Leu His Thr
225                 230                 235                 240

Val Asp His Tyr Asp Gln His Leu Thr Leu Gln Gly Leu Arg Leu Val
                245                 250                 255

Phe Gln Arg Asn Leu Gln Val Gln Arg Gly Arg Leu Tyr Thr Ala Arg
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```
                260                     265                     270




<210> 9
<211> 258
<212> PRT
<213> Bacillus subtilis

<400> 9
Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
  1               5                  10                  15

Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
             20                  25                  30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
         35                  40                  45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
     50                  55                  60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65                  70                  75                  80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
                 85                  90                  95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
            100                 105                 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
        115                 120                 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
    130                 135                 140

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145                 150                 155                 160

Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
                165                 170                 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
            180                 185                 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
        195                 200                 205

Trp Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala
    210                 215                 220

Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe
225                 230                 235                 240

Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly
                245                 250                 255

Ser Val
```

```
<210> 10
<211> 262
<212> PRT
<213> Deinococcus radiopugnans

<400> 10
Met Pro Ala Phe Pro Leu Leu Ala Val Asp Ile Gly Asn Thr Thr Thr
  1               5                  10                  15

Val Leu Gly Leu Ala Asp Ala Ser Gly Ala Leu Thr His Thr Trp Arg
             20                  25                  30

Ile Arg Thr Asn Arg Glu Met Leu Pro Asp Asp Leu Ala Leu Gln Leu
         35                  40                  45

His Gly Leu Phe Thr Leu Ala Gly Ala Pro Ile Pro Arg Ala Ala Val
     50                  55                  60

Leu Ser Ser Val Ala Pro Pro Val Gly Glu Asn Tyr Ala Leu Ala Leu
 65                  70                  75                  80

Lys Arg His Phe Met Ile Asp Ala Phe Ala Val Ser Ala Glu Asn Leu
                 85                  90                  95

Pro Asp Val Thr Val Glu Leu Asp Thr Pro Gly Ser Val Gly Ala Asp
            100                 105                 110

Arg Leu Cys Asn Leu Phe Gly Ala Glu Lys Tyr Leu Gly Gly Leu Asp
        115                 120                 125

Tyr Ala Val Val Val Asp Phe Gly Thr Ser Thr Asn Phe Asp Val Val
    130                 135                 140

Gly Arg Gly Arg Arg Phe Leu Gly Gly Ile Leu Ala Thr Gly Ala Gln
145                 150                 155                 160

Val Ser Ala Asp Ala Leu Phe Ala Arg Ala Ala Lys Leu Pro Arg Ile
                165                 170                 175

Thr Leu Gln Ala Pro Glu Thr Ala Ile Gly Lys Asn Thr Val His Ala
            180                 185                 190

Leu Gln Ser Gly Leu Val Phe Gly Tyr Ala Glu Met Val Asp Gly Leu
        195                 200                 205

Leu Arg Arg Ile Arg Ala Glu Leu Pro Gly Glu Ala Val Ala Val Ala
    210                 215                 220

Thr Gly Gly Phe Ser Arg Thr Val Gln Gly Ile Cys Gln Glu Ile Asp
225                 230                 235                 240

Tyr Tyr Asp Glu Thr Leu Thr Leu Arg Gly Leu Val Glu Leu Trp Ala
                245                 250                 255

Ser Arg Ser Glu Val Arg
            260
```

```
<210> 11
<211> 212
<212> PRT
<213> Desulfovibrio vulgaris

<400> 11
Met Thr Gln His Phe Leu Leu Phe Asp Ile Gly Asn Thr Asn Val Lys
1               5                   10                  15

Ile Gly Ile Ala Val Glu Thr Ala Val Leu Thr Ser Tyr Val Leu Pro
            20                  25                  30

Thr Asp Pro Gly Gln Thr Thr Asp Ser Ile Gly Leu Arg Leu Leu Glu
        35                  40                  45

Val Leu Arg His Ala Gly Leu Gly Pro Ala Asp Val Gly Ala Cys Val
    50                  55                  60

Ala Ser Ser Val Val Pro Gly Val Asn Pro Leu Ile Arg Arg Ala Cys
65                  70                  75                  80

Glu Arg Tyr Leu Tyr Arg Lys Leu Leu Phe Ala Pro Gly Asp Ile Ala
                85                  90                  95

Ile Pro Leu Asp Asn Arg Tyr Glu Arg Pro Ala Glu Val Gly Ala Asp
            100                 105                 110

Arg Leu Val Ala Ala Tyr Ala Ala Arg Arg Leu Tyr Pro Gly Pro Arg
        115                 120                 125

Ser Leu Val Ser Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Cys Val
    130                 135                 140

Glu Gly Gly Ala Tyr Leu Gly Gly Leu Ile Cys Pro Gly Val Leu Ser
145                 150                 155                 160

Ser Ala Gly Ala Leu Ser Ser Arg Thr Ala Lys Leu Pro Arg Ile Ser
                165                 170                 175

Leu Glu Val Glu Glu Asp Ser Pro Val Ile Gly Arg Ser Thr Thr Thr
            180                 185                 190

Ser Leu Asn His Gly Phe Ile Phe Gly Phe Ala Ala Met Thr Glu Gly
        195                 200                 205

Val Leu Ala Ala
    210


<210> 12
<211> 246
<212> PRT
<213> Thermotoga maritima

<400> 12
Met Tyr Leu Leu Val Asp Val Gly Asn Thr His Ser Val Phe Ser Ile
1               5                   10                  15

Thr Glu Asp Gly Lys Thr Phe Arg Arg Trp Arg Leu Ser Thr Gly Val
            20                  25                  30
```

```
Phe Gln Thr Glu Asp Glu Leu Phe Ser His Leu His Pro Leu Leu Gly
        35                  40                  45

Asp Ala Met Arg Glu Ile Lys Gly Ile Gly Val Ala Ser Val Val Pro
    50                  55                  60

Thr Gln Asn Thr Val Ile Glu Arg Phe Ser Gln Lys Tyr Phe His Ile
65                  70                  75                  80

Ser Pro Ile Trp Val Lys Ala Lys Asn Gly Cys Val Lys Trp Asn Val
                85                  90                  95

Lys Asn Pro Ser Glu Val Gly Ala Asp Arg Val Ala Asn Val Val Ala
            100                 105                 110

Phe Val Lys Glu Tyr Gly Lys Asn Gly Ile Ile Ile Asp Met Gly Thr
        115                 120                 125

Ala Thr Thr Val Asp Leu Val Val Asn Gly Ser Tyr Glu Gly Gly Ala
    130                 135                 140

Ile Leu Pro Gly Phe Phe Met Met Val His Ser Leu Phe Arg Gly Thr
145                 150                 155                 160

Ala Lys Leu Pro Leu Val Glu Val Lys Pro Ala Asp Phe Val Val Gly
                165                 170                 175

Lys Asp Thr Glu Glu Asn Ile Arg Leu Gly Val Val Asn Gly Ser Val
            180                 185                 190

Tyr Ala Leu Glu Gly Ile Ile Gly Arg Ile Lys Glu Val Tyr Gly Asp
        195                 200                 205

Leu Pro Val Val Leu Thr Gly Gly Gln Ser Lys Ile Val Lys Asp Met
    210                 215                 220

Ile Lys His Glu Ile Phe Asp Glu Asp Leu Thr Ile Lys Gly Val Tyr
225                 230                 235                 240

His Phe Cys Phe Gly Asp
                245


<210> 13
<211> 273
<212> PRT
<213> Treponema pallidum

<400> 13
Met Leu Leu Ile Asp Val Gly Asn Ser His Val Val Phe Gly Ile Gln
  1               5                  10                  15

Gly Glu Asn Gly Gly Arg Val Cys Val Arg Glu Leu Phe Arg Leu Ala
            20                  25                  30

Pro Asp Ala Arg Lys Thr Gln Asp Glu Tyr Ser Leu Leu Ile His Ala
        35                  40                  45

Leu Lys Glu Arg Ala Gly Val Gly Arg Ala Ser Trp Arg Asp Ala Ile
    50                  55                  60
```

```
Ile Ser Ser Val Val Pro Val Leu Thr Lys Thr Ile Ala Asp Ala Val
 65                  70                  75                  80

Ala Gln Ile Ser Gly Val Gln Pro Val Val Phe Gly Pro Trp Ala Tyr
                 85                  90                  95

Glu His Leu Pro Val Arg Ile Pro Glu Pro Val Arg Ala Glu Ile Gly
            100                 105                 110

Thr Asp Leu Val Ala Asn Ala Val Ala Ala Tyr Val His Phe Arg Ser
        115                 120                 125

Ala Cys Val Val Val Asp Cys Gly Thr Ala Leu Thr Phe Thr Ala Val
    130                 135                 140

Asp Gly Thr Gly Leu Ile Gln Gly Val Ala Ile Ala Pro Gly Leu Arg
145                 150                 155                 160

Thr Ala Val Gln Ser Leu His Thr Gly Thr Ala Gln Leu Pro Leu Val
                165                 170                 175

Pro Leu Ala Leu Pro Asp Ser Val Leu Gly Lys Asp Thr Thr His Ala
            180                 185                 190

Val Gln Ala Gly Val Val Arg Gly Thr Leu Phe Val Ile Arg Ala Met
        195                 200                 205

Ile Ala Gln Cys Gln Lys Glu Leu Gly Cys Arg Cys Ala Ala Val Ile
    210                 215                 220

Thr Gly Gly Leu Ser Arg Leu Phe Ser Ser Glu Val Asp Phe Pro Pro
225                 230                 235                 240

Ile Asp Ala Gln Leu Thr Leu Ser Gly Leu Ala His Ile Ala Arg Leu
                245                 250                 255

Val Pro Thr Ser Leu Leu Pro Pro Ala Thr Val Ser Gly Ser Ser Gly
            260                 265                 270

Asn


<210> 14
<211> 262
<212> PRT
<213> Borrelia burgdorferi

<400> 14
Met Asn Lys Pro Leu Leu Ser Glu Leu Ile Ile Asp Ile Gly Asn Thr
  1               5                  10                  15

Ser Ile Ala Phe Ala Leu Phe Lys Asp Asn Gln Val Asn Leu Phe Ile
             20                  25                  30

Lys Met Lys Thr Asn Leu Met Leu Arg Tyr Asp Glu Val Tyr Ser Phe
         35                  40                  45

Phe Glu Gly Asn Phe Asp Phe Asn Val Asn Lys Val Phe Ile Ser Ser
     50                  55                  60
```

```
Val Val Pro Ile Leu Asn Glu Thr Phe Lys Asn Val Ile Phe Ser Phe
 65                  70                  75                  80

Phe Lys Ile Lys Pro Leu Phe Ile Gly Phe Asp Leu Asn Tyr Asp Leu
                 85                  90                  95

Thr Phe Asn Pro Tyr Lys Ser Asp Lys Phe Leu Leu Gly Ser Asp Val
            100                 105                 110

Phe Ala Asn Leu Val Ala Ala Ile Glu Asn Tyr Ser Phe Glu Asn Val
        115                 120                 125

Leu Val Val Asp Leu Gly Thr Ala Cys Thr Ile Phe Ala Val Ser Arg
    130                 135                 140

Gln Asp Gly Ile Leu Gly Gly Ile Ile Asn Ser Gly Pro Leu Ile Asn
145                 150                 155                 160

Phe Asn Ser Leu Leu Asp Asn Ala Tyr Leu Ile Lys Lys Phe Pro Ile
                165                 170                 175

Ser Thr Pro Asn Asn Leu Leu Glu Arg Thr Thr Ser Gly Ser Val Asn
            180                 185                 190

Ser Gly Leu Phe Tyr Gln Tyr Lys Tyr Leu Ile Glu Gly Val Tyr Arg
        195                 200                 205

Asp Ile Lys Gln Met Tyr Lys Lys Lys Phe Asn Leu Ile Ile Thr Gly
    210                 215                 220

Gly Asn Ala Asp Leu Ile Leu Ser Leu Ile Glu Ile Glu Phe Ile Phe
225                 230                 235                 240

Asn Ile His Leu Thr Val Glu Gly Val Arg Ile Leu Gly Asn Ser Ile
                245                 250                 255

Asp Phe Lys Phe Val Asn
            260


<210> 15
<211> 229
<212> PRT
<213> Aquifex aeolicus

<400> 15
Met Arg Phe Leu Thr Val Asp Val Gly Asn Ser Ser Val Asp Ile Ala
  1               5                  10                  15

Leu Trp Glu Gly Lys Lys Val Lys Asp Phe Leu Lys Leu Ser His Glu
             20                  25                  30

Glu Phe Leu Lys Glu Glu Phe Pro Lys Leu Lys Ala Leu Gly Ile Ser
         35                  40                  45

Val Lys Gln Ser Phe Ser Glu Lys Val Arg Gly Lys Ile Pro Tyr Ile
     50                  55                  60

Lys Phe Leu Lys Lys Glu Asn Phe Pro Ile Gln Val Asp Tyr Lys Thr
 65                  70                  75                  80
```

```
Pro Glu Thr Leu Gly Thr Asp Arg Val Ala Leu Ala Tyr Ser Ala Lys
                 85                  90                  95

Lys Phe Tyr Gly Lys Asn Val Val Val Ile Ser Ala Gly Thr Ala Leu
            100                 105                 110

Val Ile Asp Leu Val Leu Glu Gly Lys Phe Lys Gly Gly Phe Ile Thr
        115                 120                 125

Leu Gly Leu Gly Lys Lys Leu Lys Ile Leu Ser Asp Leu Ala Glu Gly
    130                 135                 140

Ile Pro Glu Phe Phe Pro Glu Glu Val Glu Ile Phe Leu Gly Arg Ser
145                 150                 155                 160

Thr Arg Glu Cys Val Leu Gly Gly Ala Tyr Arg Glu Ser Thr Glu Phe
                165                 170                 175

Ile Lys Ser Thr Leu Lys Leu Trp Arg Lys Val Phe Lys Arg Lys Phe
            180                 185                 190

Lys Val Val Ile Thr Gly Gly Glu Gly Lys Tyr Phe Ser Lys Phe Gly
        195                 200                 205

Ile Tyr Asp Pro Leu Leu Val His Arg Gly Met Arg Asn Leu Leu Tyr
    210                 215                 220

Leu Tyr His Arg Ile
225


<210> 16
<211> 257
<212> PRT
<213> Synechocystis sp.

<400> 16
Met Glu Thr Ser Lys Pro Gly Cys Gly Leu Ala Leu Asp Asn Asp Lys
  1               5                  10                  15

Gln Lys Pro Trp Leu Gly Leu Met Ile Gly Asn Ser Arg Leu His Trp
             20                  25                  30

Ala Tyr Cys Ser Gly Asn Ala Pro Leu Gln Thr Trp Val Thr Asp Tyr
         35                  40                  45

Asn Pro Lys Ser Ala Gln Leu Pro Val Leu Leu Gly Lys Val Pro Leu
     50                  55                  60

Met Leu Ala Ser Val Val Pro Glu Gln Thr Glu Val Trp Arg Val Tyr
 65                  70                  75                  80

Gln Pro Lys Ile Leu Thr Leu Lys Asn Leu Pro Leu Val Asn Leu Tyr
                 85                  90                  95

Pro Ser Phe Gly Ile Asp Arg Ala Leu Ala Gly Leu Gly Thr Gly Leu
            100                 105                 110

Thr Tyr Gly Phe Pro Cys Leu Val Val Asp Gly Gly Thr Ala Leu Thr
        115                 120                 125
```

```
Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
    130                 135                 140

Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
145                 150                 155                 160

Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
                165                 170                 175

Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
            180                 185                 190

Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro
        195                 200                 205

Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly
    210                 215                 220

Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn
225                 230                 235                 240

Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile
                245                 250                 255

Cys


<210> 17
<211> 223
<212> PRT
<213> Helicobacter pylori

<400> 17
Met Pro Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
1               5                   10                  15

Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
            20                  25                  30

Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
        35                  40                  45

Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
    50                  55                  60

Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Glu Thr Asp
65                  70                  75                  80

Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
                85                  90                  95

Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
            100                 105                 110

Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Pro Gly Leu Ala Gln
        115                 120                 125

Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Glu Gln Pro Phe
    130                 135                 140
```

```
Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
145                 150                 155                 160

Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
                165                 170                 175

Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
            180                 185                 190

Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
        195                 200                 205

Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
    210                 215                 220


<210> 18
<211> 267
<212> PRT
<213> Bordetella pertussis

<400> 18
Met Ile Ile Leu Ile Asp Ser Gly Asn Ser Arg Leu Lys Val Gly Trp
  1               5                  10                  15

Phe Asp Pro Asp Ala Pro Gln Ala Ala Arg Glu Pro Ala Pro Val Ala
            20                  25                  30

Phe Asp Asn Leu Asp Leu Asp Ala Leu Gly Arg Trp Leu Ala Thr Leu
        35                  40                  45

Pro Arg Arg Pro Gln Arg Ala Leu Gly Val Asn Val Ala Gly Leu Ala
    50                  55                  60

Arg Gly Glu Ala Ile Ala Ala Thr Leu Arg Ala Gly Gly Cys Asp Ile
 65                  70                  75                  80

Arg Trp Leu Arg Ala Gln Pro Leu Ala Met Gly Leu Arg Asn Gly Tyr
                 85                  90                  95

Arg Asn Pro Asp Gln Leu Gly Ala Asp Arg Trp Ala Cys Met Val Gly
            100                 105                 110

Val Leu Ala Arg Gln Pro Ser Val His Pro Pro Leu Leu Val Ala Ser
        115                 120                 125

Phe Gly Thr Ala Thr Thr Leu Asp Thr Ile Gly Pro Asp Asn Val Phe
    130                 135                 140

Pro Gly Gly Leu Ile Leu Pro Gly Pro Ala Met Met Arg Gly Ala Leu
145                 150                 155                 160

Ala Tyr Gly Thr Ala His Leu Pro Leu Ala Asp Gly Leu Val Ala Asp
                165                 170                 175

Tyr Pro Ile Asp Thr His Gln Ala Ile Ala Ser Gly Ile Ala Ala Ala
            180                 185                 190

Gln Ala Gly Ala Ile Val Arg Gln Trp Leu Ala Gly Arg Gln Arg Tyr
        195                 200                 205
```

```
Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
    210                 215                 220

Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
225                 230                 235                 240

Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu
                245                 250                 255

Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
            260                 265


<210> 19
<211> 777
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(774)

<400> 19
ttg tta ctg gtt atc gat gtg ggg aac acc aat act gta ctt ggt gta      48
Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
1               5                   10                  15

tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg      96
Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
            20                  25                  30

cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat     144
His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
        35                  40                  45

cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tcg tca     192
His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
    50                  55                  60

gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac     240
Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65                  70                  75                  80

ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta     288
Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
                85                  90                  95

aat ata aaa tat gac aat ccg aaa gaa gta ggg gca gac aga atc gta     336
Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
            100                 105                 110

aat gct gtc gct gcg ata cac ttg tat ggc aat cca tta att gtt gtc     384
Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
        115                 120                 125

gat ttc gga act gct act act tat tgc tat att gat gaa aat aaa caa     432
Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
    130                 135                 140

tac atg ggc ggc gcg att gcg att ggc ata aca att tct aca [illegible] gcg     480
Tyr Met Gly Gly Ala Ile Ala Ile Gly Ile Thr Ile Ser Thr [illegible] Ala
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145 150 155 160

ctt tac tcg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc 528
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
165 170 175

gac aat att atc gga aaa aac act gtt agc gcg atg caa tct gga att 576
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
180 185 190

tta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag cga atg aaa 624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
195 200 205

tgg cag gca aaa cag gac ctc aag gtc att gcg aca gga ggc ctg gcg 672
Trp Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala
210 215 220

ccg ctt att gcg aac gaa tca gat tgt ata gac atc gtt gat cca ttc 720
Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe
225 230 235 240

tta acc cta aaa ggg ctg gaa ttg att tat gaa aga aac cgc gta gga 768
Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly
245 250 255

agt gta tag 777
Ser Val

<210> 20
<211> 960
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(957)

<400> 20
gtg aaa aat aaa gaa ctt aac cta cat act tta tat aca cag cac aat 48
Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
1 5 10 15

cgg gag tct tgg tct ggt ttt ggg gga cat ttg tcg att gct gta tct 96
Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
20 25 30

gaa gaa gag gca aaa gct gtg gaa gga ttg aat gat tat cta tct gtt 144
Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
35 40 45

gaa gaa gtg gag acg att tat att ccg ctt gtt cgc tta ctt cat tta 192
Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu
50 55 60

cat gtc aag tct gca gct gaa cgt aac aaa cat gtc aat gtt ttt ttg 240
His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
65 70 75 80

[illegible]

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Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
                 85                  90                  95

agt gtc gca gtc gga aaa agc acg acg gcg cgg atc ttg cag aag ctg    336
Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
            100                 105                 110

ctt tcg cgt ttg cct gac cgt cca aaa gtg agc ctt atc acg aca gat    384
Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
        115                 120                 125

ggt ttt tta ttt cct act gcc gag ctg aaa aag aaa aat atg atg tca    432
Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
    130                 135                 140

aga aaa gga ttt cct gaa agc tat gat gta aag gcg ctg ctc gaa ttt    480
Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
145                 150                 155                 160

ttg aat gac tta aaa tca gga aag gac agc gta aag gcc ccg gtg tat    528
Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
                165                 170                 175

tcc cat cta acc tat gac cgc gag gaa ggt gtg ttc gag gtt gta gaa    576
Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
            180                 185                 190

cag gcg gat att gtg att att gaa ggc att aat gtt ctt cag tcg ccc    624
Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
        195                 200                 205

acc ttg gag gat gac cgg gaa aac ccg cgt att ttt gtt tcc gat ttc    672
Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
    210                 215                 220

ttt gat ttt tcg att tat gtg gat gcg gag gaa agc cgg att ttc act    720
Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
225                 230                 235                 240

tgg tat tta gag cgt ttt cgc ctg ctt cgg gaa aca gct ttt caa aat    768
Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
                245                 250                 255

cct gat tca tat ttt cat aaa ttt aaa gac ttg tcc gat cag gag gct    816
Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
            260                 265                 270

gac gag atg gca gcc tcg att tgg gag agt gtc aac cgg ccg aat tta    864
Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
        275                 280                 285

tat gaa aat att ttg cca act aaa ttc agg tca gat ctc att ttg cgt    912
Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
    290                 295                 300

aaa gga gat ggg cat aaa gtt gaa gaa gtc ttg gta agg agg gta tga    960
Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
305                 310                 315
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<211> 882
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(879)

<400> 21
ttg tcg att gct gta tct gaa gaa gag gca aaa gct gtg gaa gga ttg      48
Met Ser Ile Ala Val Ser Glu Glu Glu Ala Lys Ala Val Glu Gly Leu
 1               5                  10                  15

aat gat tat cta tct gtt gaa gaa gtg gag acg atc tat att ccg ctt      96
Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu
            20                  25                  30

gtt cgc ttg ctt cat tta cat gtc aag tct gcg gct gaa cgc aat aag     144
Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
        35                  40                  45

cat gtc aat gtt ttt ttg aag cac cca cat tca gcc aaa att ccg ttt     192
His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
    50                  55                  60

att atc ggc att gcc ggc agt gtc gca gtc gga aaa agc acg acg gcg     240
Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
65                  70                  75                  80

cgg atc ttg cag aag ctg ctt tcg cgt ttg cct gac cgt cca aaa gtg     288
Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
                85                  90                  95

agc ctt atc acg aca gat ggt ttt tta ttt cct act gcc gag ctg aaa     336
Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
            100                 105                 110

aag aaa aat atg atg tca aga aaa gga ttt cct gaa agc tat gat gta     384
Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val
        115                 120                 125

aag gcg ctg ctc gaa ttt ttg aat gac tta aaa tca gga aag gac agc     432
Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
    130                 135                 140

gta aag gcc ccg gtg tat tcc cat tta acc tat gac cgc gag gaa ggt     480
Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
145                 150                 155                 160

gtg ttc gag gtt gta gaa cag gcg gat att gtg att att gaa ggc att     528
Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
                165                 170                 175

aat gtt ctt cag tcg ccc acc ttg gag gat gat cgg gaa aat ccg cgt     576
Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
            180                 185                 190

att ttt gtt tcc gat ttt ttt gat ttt tcg att tat gtg gat gcg gaa     624
Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu
        195                 200                 205
```

```
gaa agc cgg att ttc act tgg tat tta gag cgt ttt cgc ctg ctt cgg     672
Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
    210                 215                 220

gaa aca gct ttt caa aat cct gat tca tat ttt cat aaa ttt aaa gac     720
Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
225                 230                 235                 240

ttg tcc gat cag gag gct gac gag atg gca gcc tcg att tgg gag agt     768
Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
                245                 250                 255

gtc aac cgg ccg aat tta tat gaa aat att ttg cca act aaa ttc agg     816
Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
            260                 265                 270

tca gat ctc att ttg cgt aag gga gac ggg cat aag gtc gag gaa gtg     864
Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
        275                 280                 285

ttg gta agg agg gta tga                                             882
Leu Val Arg Arg Val
    290


<210> 22
<211> 846
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(843)

<400> 22
gtg gaa gga ttg aat gat tat cta tct gtt gaa gaa gtg gag acg atc     48
Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile
  1               5                  10                  15

tat att ccg ctt gtt cgc ttg ctt cat tta cat gtc aag tct gcg gct     96
Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala
                 20                  25                  30

gaa cgc aat aag cat gtc aat gtt ttt ttg aag cac cca cat tca gcc     144
Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
            35                  40                  45

aaa att ccg ttt att att ggc att gct ggc agt gtc gca gtc gga aaa     192
Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
    50                  55                  60

agc acg acg gcg cgg att ttg cag aag ctg ctt tcg cgt ttg cct gac     240
Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
65                  70                  75                  80

[illegible]                                                         288
Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Ile Leu Phe Pro Thr
                85                  90                  95

[illegible]                                                         336
Ala Glu Leu Lys Lys Lys Asn Met Met Ser Ala Tyr Gly Phe Pro Glu
```

```
            100                     105                     110

agc tat gat gta aag gcg ctg ctc gaa ttt ttg aat gac tta aaa tca      384
Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser
        115                 120                 125

gga aag gac agc gta aag gcc ccg gtg tat tcc cat cta acc tat gac      432
Gly Lys Asp Ser Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp
    130                 135                 140

cgc gag gaa ggt gtg ttc gag gtt gta gaa cag gcg gat att gtg att      480
Arg Glu Glu Gly Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile
145                 150                 155                 160

att gaa ggc att aat gtt ctt cag tcg ccc acc ttg gag gat gac cgg      528
Ile Glu Gly Ile Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg
                165                 170                 175

gaa aac ccg cgt att ttt gtt tcc gat ttc ttt gat ttt tcg att tat      576
Glu Asn Pro Arg Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr
            180                 185                 190

gtg gat gcg gag gaa agc cgg att ttc act tgg tat tta gag cgt ttt      624
Val Asp Ala Glu Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe
        195                 200                 205

cgc ctg ctt cgg gaa aca gct ttt caa aat cct gat tca tat ttt cat      672
Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His
    210                 215                 220

aaa ttt aaa gac ttg tcc gat cag gag gct gac gag atg gca gcc tcg      720
Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser
225                 230                 235                 240

att tgg gag agt gtc aac cgg ccg aat tta tat gaa aat att ttg cca      768
Ile Trp Glu Ser Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro
                245                 250                 255

act aaa ttc agg tca gat ctc att ttg cgt aag gga gac ggg cat aag      816
Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys
            260                 265                 270

gtc gag gaa gtg ttg gta agg agg gta tga                              846
Val Glu Glu Val Leu Val Arg Arg Val
        275                 280


<210> 23
<211> 831
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(831)

<400> 23
[illegible]                                                           48
Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pr
1               5                   10                  15
```

```
att gtc atg ctg acc gct tat gat tat ccg gca gct aaa ctt gct gaa     96
Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
             20                  25                  30

caa gcg gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc     144
Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
         35                  40                  45

gtc ctc ggc ctt gat tca act gtc ggt gtg aca gtt gcg gac atg atc     192
Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
     50                  55                  60

cat cat aca aaa gcc gtt aaa agg ggt gcg ccg aat acc ttt att gtg     240
His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
 65                  70                  75                  80

aca gat atg ccg ttt atg tct tat cac ctg tct aag gaa gat acg ctg     288
Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
                 85                  90                  95

aaa aat gca gcg gct atc gtt cag gaa agc gga gct gac gca ctg aag     336
Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys
            100                 105                 110

ctt gag ggc gga gaa ggc gtg ttt gaa tcc att cgc gca ttg acg ctt     384
Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu
        115                 120                 125

gga ggc att cca gta gtc agt cac tta ggt ttg aca ccg cag tca gtc     432
Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val
    130                 135                 140

ggc gta ttg gga ggc tat aaa gta cag ggc aaa gac gaa caa agt gcc     480
Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala
145                 150                 155                 160

aaa aaa tta ata gaa gac agt ata aaa tgc gaa gaa gca gga gct atg     528
Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met
                165                 170                 175

atg ctt gtg ctg gaa tgt gtg ccg gca gaa ctc aca gct aaa att gcc     576
Met Leu Val Leu Glu Cys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala
            180                 185                 190

gag acg cta agc ata ccg gtc att gga atc ggc gct ggt gtg aaa gcg     624
Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala
        195                 200                 205

gac gga caa gtt ctc gtt tat cat gat att atc ggc cac ggt gtt gag     672
Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu
    210                 215                 220

aga aca cct aaa ttt gta aaa caa tat acg cgt att gat gaa act atc     720
Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile
225                 230                 235                 240

gaa aca gca att agc gga tat gtt caa gat gta aga cat cgt gct ttc     768
Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe
                245                 250                 255

[illegible]                                                          816
```

```
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
            260                 265                 270

ttg tac ggg gga aaa                                                 831
Leu Tyr Gly Gly Lys
        275


<210> 24
<211> 277
<212> PRT
<213> Bacillus subtilis

<400> 24
Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
1               5                   10                  15

Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
            20                  25                  30

Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
        35                  40                  45

Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
    50                  55                  60

His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
65                  70                  75                  80

Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
                85                  90                  95

Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys
            100                 105                 110

Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu
        115                 120                 125

Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val
    130                 135                 140

Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala
145                 150                 155                 160

Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met
                165                 170                 175

Met Leu Val Leu Glu Cys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala
            180                 185                 190

Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala
        195                 200                 205

Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu
    210                 215                 220

Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile
225                 230                 235                 240

Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe
                245                 250                 255
```

```
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
            260                 265                 270

Leu Tyr Gly Gly Lys
        275


<210> 25
<211> 858
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(858)

<400> 25
atg aga cag att act gat att tca cag ctg aaa gaa gcc ata aaa caa      48
Met Arg Gln Ile Thr Asp Ile Ser Gln Leu Lys Glu Ala Ile Lys Gln
  1               5                  10                  15

tac cat tca gag ggc aag tca atc gga ttt gtt ccg acg atg ggg ttt      96
Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
            20                  25                  30

ctg cat gag ggg cat tta acc tta gca gac aaa gca aga caa gaa aac     144
Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
        35                  40                  45

gac gcc gtt att atg agt att ttt gtg aat cct gca caa ttc ggc cct     192
Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
    50                  55                  60

aat gaa gat ttt gaa gca tat ccg cgc gat att gag cgg gat gca gct     240
Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65                  70                  75                  80

ctt gca gaa aac gcc gga gtc gat att ctt ttt acg cca gat gct cat     288
Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
                 85                  90                  95

gat atg tat ccc ggt gaa aag aat gtc acg att cat gta gaa aga cgc     336
Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
            100                 105                 110

acg gac gtg tta tgc ggg cgc tca aga gaa gga cat ttt gat ggg gtc     384
Thr Asp Val Leu Cys Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
        115                 120                 125

gca atc gta ttg acg aag ctt ttc aat cta gtc aag ccg act cgt gcc     432
Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
    130                 135                 140

tat ttc ggt tta aaa gat gcg cag cag gtg gct gtt gtt gat ggg tta     480
Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu
145                 150                 155                 160

att agc gat att ttc atg gat att gaa ctt gtt ccc gtg gat acg gtg     528
Ile Ser Asp Ile Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val
                165                 170                 175
```

```
aga gag gaa gac ggc tta gcc aaa agc tct cgc aat gta tac tta aca      576
Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
            180                 185                 190

gct gag gaa aga aaa gaa gcg cct aag ctg tat cgg gcc ctt caa aca      624
Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr
        195                 200                 205

agt gcg gaa ctt gtc caa gcc ggt gaa aga gat cct gaa gcg gtg ata      672
Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
    210                 215                 220

aaa gct gca aaa gat atc att gaa acg act agc gga acc ata gac tat      720
Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
225                 230                 235                 240

gta gag ctt tat tcc tat ccg gaa ctc gag cct gtg aat gaa att gct      768
Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
                245                 250                 255

gga aag atg att ctc gct gtt gca gtt gct ttt tca aaa gcg cgt tta      816
Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
            260                 265                 270

ata gat aat atc att att gat att cga gaa atg gag aga ata              858
Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
        275                 280                 285


<210> 26
<211> 286
<212> PRT
<213> Bacillus subtilis

<400> 26
Met Arg Gln Ile Thr Asp Ile Ser Gln Leu Lys Glu Ala Ile Lys Gln
  1               5                  10                  15

Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
            20                  25                  30

Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
        35                  40                  45

Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
    50                  55                  60

Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65                  70                  75                  80

Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
                 85                  90                  95

Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
            100                 105                 110

Thr Asp Val Leu Cys Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
        115                 120                 125

Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
```

130 135 140

Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu
145 150 155 160

Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val
165 170 175

Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
180 185 190

Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr
195 200 205

Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
210 215 220

Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
225 230 235 240

Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
245 250 255

Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
260 265 270

Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
275 280 285

<210> 27
<211> 381
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(381)

<400> 27
atg tat cga aca atg atg agc ggc aaa ctt cac agg gca act gtt acg 48
Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr
1 5 10 15

gaa gca aac ctg aac tat gtg gga agc att aca att gat gaa gat ctc 96
Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu
20 25 30

att gat gct gtg gga atg ctt cct aat gaa aaa gta caa att gtg aat 144
Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
35 40 45

aat aat aat gga gca cgt ctt gaa acg tat att att cct ggt aaa cgc 192
Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile Ile Pro Gly Lys Arg
50 55 60

[illegible] 240
Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
65 70 75 80

[illegible] 288

```
Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
                85                  90                  95

gaa gcg gca agc cat gag ccg aaa gtg gct gtt ctg aat gat caa aac      336
Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
            100                 105                 110

aaa att gaa caa atg ctg ggg aac gaa cca gcc cgt aca att ttg          381
Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
        115                 120                 125


<210> 28
<211> 127
<212> PRT
<213> Bacillus subtilis

<400> 28
Met Tyr Arg Thr Met Met Ser Gly Lys Leu His Arg Ala Thr Val Thr
1               5                   10                  15

Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu
            20                  25                  30

Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
        35                  40                  45

Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile Ile Pro Gly Lys Arg
    50                  55                  60

Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
65                  70                  75                  80

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
                85                  90                  95

Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
            100                 105                 110

Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
        115                 120                 125


<210> 29
<211> 894
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(894)

<400> 29
atg aaa att gga att atc [illegible]                                  48
Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Tyr Ala
1               5                   10                  15

[illegible]                                                          96
Tyr Tyr Leu Ser Leu Tyr His Asp Val Thr Val Val Thr Arg Arg Gln
            20                  25                  30
```

```
gaa cag gct gcg gcc att cag tct gaa gga atc cgg ctt tat aaa ggc      144
Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
         35                  40                  45

ggg gag gaa ttc agg gct gat tgc agt gcg gat acg agt atc aat tcg      192
Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser
     50                  55                  60

gac ttt gac ctg ctt gtc gtg aca gtg aag cag cat cag ctt caa tct      240
Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
 65                  70                  75                  80

gtt ttt tcg tcg ctt gaa cga atc ggg aag acg aat ata tta ttt ttg      288
Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
                 85                  90                  95

caa aac ggc atg ggg cat atc cac gac cta aaa gac tgg cac gtt ggc      336
Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
            100                 105                 110

cat tcc att tat gtt gga atc gtt gag cac gga gct gta aga aaa tcg      384
His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
        115                 120                 125

gat aca gct gtt gat cat aca ggc cta ggt gcg ata aaa tgg agc gcg      432
Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
    130                 135                 140

ttc gac gat gct gaa cca gac cgg ctg aac atc ttg ttt cag cat aac      480
Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn
145                 150                 155                 160

cat tcg gat ttt ccg att tat tat gag acg gat tgg tac cgt ctg ctg      528
His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu
                165                 170                 175

acg ggc aag ctg att gta aat gcg tgt att aat cct tta act gcg tta      576
Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu
            180                 185                 190

ttg caa gtg aaa aat gga gaa ctg ctg aca acg cca gct tat ctg gct      624
Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala
        195                 200                 205

ttt atg aag ctg gta ttt cag gag gca tgc cgc att tta aaa ctt gaa      672
Phe Met Lys Leu Val Phe Gln Glu Ala Cys Arg Ile Leu Lys Leu Glu
    210                 215                 220

aat gaa gaa aag gct tgg gag cgg gtt cag gcc gtt tgt ggg caa acg      720
Asn Glu Glu Lys Ala Trp Glu Arg Val Gln Ala Val Cys Gly Gln Thr
225                 230                 235                 240

aaa gag aat cgt tca tca atg ctg gtt gac gtc att gga ggc cgg cag      768
Lys Glu Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln
                245                 250                 255

acg gaa gct gat gct att att gga tat tta ttg aaa gaa gca agt ctt      816
Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu
            260                 265                 270

[illegible]                                                          864
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Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
        275                 280                 285

gca ttg gag cga aat aca aac aaa gtc ttt                               894
Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
    290                 295


<210> 30
<211> 298
<212> PRT
<213> Bacillus subtilis

<400> 30
Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Cys Ala
  1               5                  10                  15

Tyr Tyr Leu Ser Leu Tyr His Asp Val Thr Val Val Thr Arg Arg Gln
             20                  25                  30

Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
         35                  40                  45

Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser
     50                  55                  60

Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
 65                  70                  75                  80

Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
                 85                  90                  95

Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
            100                 105                 110

His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
        115                 120                 125

Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
    130                 135                 140

Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn
145                 150                 155                 160

His Ser Asp Phe Pro Ile Tyr Tyr Glu Thr Asp Trp Tyr Arg Leu Leu
                165                 170                 175

Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu
            180                 185                 190

Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala
        195                 200                 205

Phe Met Lys Leu Val Phe Gln Glu Ala Cys Arg Ile Leu Lys Leu Glu
    210                 215                 220

Asn Glu Glu Lys Ala Trp Glu Arg Val Gln Ala Val Cys Gly Gln Thr
225                 230                 235                 240

Lys Glu Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln
                245                 250                 255
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```
Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu
            260                 265                 270

Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
        275                 280                 285

Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
    290                 295


<210> 31
<211> 1725
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1722)

<400> 31
atg ggg act aat gta cag gtg gat tca gca tct gcc gaa tgt aca cag      48
Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln
1               5                   10                  15

acg atg agc gga gca tta atg ctg att gaa tca tta aaa aaa gag aaa      96
Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys
            20                  25                  30

gta gaa atg att ttc ggt tat ccg ggc ggg gct gtg ctt cca att tac     144
Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
        35                  40                  45

gat aag cta tat aat tca ggg ttg gta cat att ctt ccc cgt cat gaa     192
Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
    50                  55                  60

caa gga gca att cat gca gcg gag gga tac gca agg gtc tcc gga aaa     240
Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
65                  70                  75                  80

cca ggt gtc gtc att gcc acg tca ggg ccg gga gcg aca aac ctt gtt     288
Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
                85                  90                  95

aca ggc ctt gct gat gcc atg att gat tca ttg ccg tta gtt gtt ttt     336
Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
            100                 105                 110

aca ggg cag gta gca acc tct gta atc ggg agc gat gca ttt cag gaa     384
Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu
        115                 120                 125

gca gac att tta ggg att acg atg cca gta aca aaa cat agc tac caa     432
Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln
    130                 135                 140

gtt cgt caa ccg gaa gat ttg ccg cgt att att aaa gaa gct ttt cat     480
Val Arg Gln Pro Glu Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His
145                 150                 155                 160
```

```
att gca aca act gga aga ccc gga cct gta ttg att gat att ccg aaa      528
Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys
                165                 170                 175

gat gta gca aca att gaa gga gaa ttc agc tat gat cat gag atg aat      576
Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn
            180                 185                 190

ctc ccg gga tac cag ccg aca aca gag ccg aat tat ttg cag atc cgc      624
Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg
        195                 200                 205

aag ctt gtg gaa gcc gtg agc agt gcg aaa aaa ccg gtg atc ctg gcg      672
Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala
    210                 215                 220

ggt gcg ggc gta ctg cac gga aaa gcg tca gaa gaa tta aaa aat tat      720
Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr
225                 230                 235                 240

gct gaa cag cag caa atc cct gtg gca cac acc ctt ttg ggg ctc gga      768
Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly
                245                 250                 255

ggc ttc ccg gct gac cat ccg ctt ttc cta ggg atg gcg gga atg cac      816
Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His
            260                 265                 270

ggt act tat aca gcc aat atg gcc ctt cat gaa tgt gat cta tta atc      864
Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile
        275                 280                 285

agt att ggc gcc cgt ttt gat gac cgt gtc aca gga aac ctg aaa cac      912
Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His
    290                 295                 300

ttt gcc aga aac gca aag ata gcc cac atc gat att gat cca gct gaa      960
Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu
305                 310                 315                 320

atc gga aaa atc atg aaa aca caa att cct gta gtc gga gac agc aaa      1008
Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys
                325                 330                 335

att gtc ctg cag gaa ctg atc aaa caa gac ggc aaa caa agc gat tca      1056
Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser
            340                 345                 350

agc gaa tgg aaa aaa cag ctc gca gaa tgg aaa gaa gag tat ccg ctc      1104
Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu
        355                 360                 365

tgg tat gtc gat aat gaa gaa gaa ggt ttt aaa cct cag aaa ttg att      1152
Trp Tyr Val Asp Asn Glu Glu Glu Gly Phe Lys Pro Gln Lys Leu Ile
    370                 375                 380

gaa tat att cat caa ttt aca aaa gga gaa gcc att gtc gca acg gat      1200
Glu Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp
385                 390                 395                 400

gta ggc cag cat caa atg tgg tca gcg caa ttt tat ccg ttc caa gaa      1248
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```
Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
                405                 410                 415

gca gat aaa tgg gtc acg tca ggc gga ctt gga acg atg gga ttc ggt      1296
Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
            420                 425                 430

ctt ccg gcg gcg atc ggc gca cag ctg gcc gaa aaa gat gct act gtt      1344
Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val
        435                 440                 445

gtc gcg gtt gtc gga gac ggc gga ttc caa atg acg ctt caa gaa ctc      1392
Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
    450                 455                 460

gat gtt att cgc gaa tta aat ctt ccg gtc aag gta gtg att tta aat      1440
Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
465                 470                 475                 480

aac gct tgt ctc gga atg gtc aga cag tgg cag gaa att ttc tat gaa      1488
Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
                485                 490                 495

gaa cgt tat tca gaa tct aaa ttc gct tct cag cct gac ttc gtc aaa      1536
Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
            500                 505                 510

ttg tcc gaa gca tac ggc att aaa ggc atc aga att tca tca gaa gcg      1584
Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
        515                 520                 525

gaa gca aag gaa aag ctg gaa gag gca tta aca tca aga gaa cct gtt      1632
Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val
    530                 535                 540

gtc att gac gtg cgg gtt gcc agc gaa gaa aaa gta ttc ccg atg gtg      1680
Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
545                 550                 555                 560

gct ccg ggg aaa ggg ctg cat gaa atg gtg ggg gtg aaa cct tga          1725
Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro
                565                 570


<210> 32
<211> 574
<212> PRT
<213> Bacillus subtilis

<400> 32
Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln
  1               5                  10                  15

Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys
            20                  25                  30

Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
        35                  40                  45

Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
    50                  55                  60
```

```
Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
 65                  70                  75                  80

Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
                 85                  90                  95

Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
            100                 105                 110

Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu
        115                 120                 125

Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln
    130                 135                 140

Val Arg Gln Pro Glu Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His
145                 150                 155                 160

Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys
                165                 170                 175

Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn
            180                 185                 190

Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg
        195                 200                 205

Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala
    210                 215                 220

Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr
225                 230                 235                 240

Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly
                245                 250                 255

Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His
            260                 265                 270

Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile
        275                 280                 285

Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His
    290                 295                 300

Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu
305                 310                 315                 320

Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys
                325                 330                 335

Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser
            340                 345                 350

Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu
        355                 360                 365

Trp Tyr Val Asp Asn Glu Gly Glu Gly Phe Lys Pro Gln Lys Leu Glu
    370                 375                 380
```

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Glu Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp
385                 390                 395                 400

Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
                405                 410                 415

Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
            420                 425                 430

Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val
        435                 440                 445

Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
    450                 455                 460

Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
465                 470                 475                 480

Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
                485                 490                 495

Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
            500                 505                 510

Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
        515                 520                 525

Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val
    530                 535                 540

Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
545                 550                 555                 560

Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro
                565                 570


<210> 33
<211> 525
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(522)

<400> 33
ttg aaa aga att atc aca ttg act gtg gtg aac cg[illegible] [illegible] [illegible] [illegible] tta      48
Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu
  1               5                  10                  15

aac cgg atc acc ggt cta ttc aca aaa agg cat tac aac att gaa agc      96
Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
             20                  25                  30

[illegible]                                                         144
Ile Thr Val Gly His Thr [illegible] Thr Ala Gly Val Ser Arg Ile Thr Phe
         35                  40                  45

[illegible]                                                         192
Val Val His Val [illegible] Gly [illegible] Asn Asp Val [illegible] [illegible] [illegible] Thr Lys [illegible]
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    50                  55                  60

ctc aac aaa cag att gat gtg ctg aaa gtc aca gac atc aca aat caa      240
Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65                 70                  75                  80

tcg att gtc cag agg gag ctg gcc tta atc aag gtt gtc tcc gca cct      288
Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro
                85                  90                  95

tca aca aga aca gag att aat gga atc ata gaa ccg ttt aga gcc tct      336
Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser
            100                 105                 110

gtc gtt gat gtc agc aga gac agc atc gtt gtt cag gtg aca ggt gaa      384
Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu
        115                 120                 125

tct aac aaa att gaa gcg ctt att gag tta tta aaa cct tat ggc att      432
Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
    130                 135                 140

aaa gaa atc gcg aga aca ggt aca acg gct ttt gcg agg gga acc agc      480
Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser
145                 150                 155                 160

aaa agg cgt cat cca ata aaa caa tat cta ttg tat aaa aca taa          525
Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
                165                 170


<210> 34
<211> 174
<212> PRT
<213> Bacillus subtilis

<400> 34
Met Lys Arg Ile Ile Thr Leu Thr Val Val Asn Arg Ser Gly Val Leu
 1               5                  10                  15

Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
            20                  25                  30

Ile Thr Val Gly His Thr Glu Thr Ala Gly Val Ser Arg Ile Thr Phe
        35                  40                  45

Val Val His Val Glu Gly Glu Asn Asp Val Glu Gln Leu Thr Lys Gln
    50                  55                  60

Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65                 70                  75                  80

Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro
                85                  90                  95

Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser
            100                 105                 110

Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu
        115                 120                 125
```

```
Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile
    130                 135                 140

Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser
145                 150                 155                 160

Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
                165                 170


<210> 35
<211> 1029
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1026)

<400> 35
atg gta aaa gta tat tat aac ggt gat atc aaa gag aac gta ttg gct      48
Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
  1               5                  10                  15

gga aaa aca gta gcg gtt atc ggg tac ggt tcg caa ggc cac gca cat      96
Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
             20                  25                  30

gcc ctg aac ctt aaa gaa agc gga gta gac gtg atc gtc ggt gtt aga     144
Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg
         35                  40                  45

caa gga aaa tct ttc act caa gcc caa gaa gat gga cat aaa gta ttt     192
Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe
     50                  55                  60

tca gta aaa gaa gcg gca gcc caa gcc gaa atc atc atg gtt ctg ctt     240
Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu
 65                  70                  75                  80

ccg gat gag cag cag caa aaa gta tac gaa gct gaa atc aaa gat gaa     288
Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Glu
                 85                  90                  95

ttg aca gca gga aaa tca tta gta ttc gct cat gga ttt aac gtg cat     336
Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His
            100                 105                 110

ttc cat caa att gtt cct ccg gcg gat gta gat gta ttc tta gtg gcc     384
Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala
        115                 120                 125

cct aaa ggc cct gga cac ttg gta aga aga aca tat gag caa gga gct     432
Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Glu Gln Gly Ala
    130                 135                 140

ggc gta cct gca ttg ttc gca atc tat caa gat gtt act ggc caa gca     480
Gly Val Pro Ala Leu Phe Ala Ile Tyr Gln Asp Val Thr Gly Gln Ala
145                 150                 155                 160

aca [illegible] aaa [illegible] [illegible] [illegible] [illegible] [illegible] aaa [illegible] [illegible] [illegible] [illegible] [illegible] [illegible] [illegible]     [illegible]
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Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala
                165                 170                 175

ggc gta tta gaa acg aca ttt aaa gaa gaa aca gaa aca gat ttg ttc     576
Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe
            180                 185                 190

ggt gag caa gca gtt ctt tgc ggc gga tta agc gcg ctt gtc aaa gcc     624
Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala
        195                 200                 205

gga ttt gaa acc tta act gaa gca ggt tat cag cct gaa ctt gca tac     672
Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr
    210                 215                 220

ttc gag tgt ctt cat gag ctg aaa tta atc gta gac ctt atg tac gaa     720
Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
225                 230                 235                 240

gaa gga ctt gca gga atg aga tat tca atc tct gac aca gca cag tgg     768
Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp
                245                 250                 255

gga gat ttc gta tca ggc cct cgc gtt gtg gac gcc aaa gta aaa gaa     816
Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu
            260                 265                 270

tct atg aaa gaa gta tta aaa gat atc caa aac ggt aca ttc gca aaa     864
Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys
        275                 280                 285

gag tgg atc gtc gaa aac caa gta aac cgt cct cgt ttc aac gct atc     912
Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile
    290                 295                 300

aat gca agc gag aac gaa cat caa atc gaa gta gtg gga aga aag ctt     960
Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu
305                 310                 315                 320

cgt gaa atg atg ccg ttt gtg aaa caa ggc aag aag aag gaa gcg gtg     1008
Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val
                325                 330                 335

gtc tcc gtt gcg caa aat taa                                         1029
Val Ser Val Ala Gln Asn
            340


<210> 36
<211> 342
<212> PRT
<213> Bacillus subtilis

<400> 36
Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala
1               5                   10                  15

Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His
            20                  25                  30

Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg
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        35                  40                  45

Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe
    50                  55                  60

Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu
65                  70                  75                  80

Pro Asp Glu Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Glu
                85                  90                  95

Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Gly Phe Asn Val His
            100                 105                 110

Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala
        115                 120                 125

Pro Lys Gly Pro Gly His Leu Val Arg Arg Thr Tyr Glu Gln Gly Ala
    130                 135                 140

Gly Val Pro Ala Leu Phe Ala Ile Tyr Gln Asp Val Thr Gly Glu Ala
145                 150                 155                 160

Arg Asp Lys Ala Leu Ala Tyr Ala Lys Gly Ile Gly Gly Ala Arg Ala
                165                 170                 175

Gly Val Leu Glu Thr Thr Phe Lys Glu Glu Thr Glu Thr Asp Leu Phe
            180                 185                 190

Gly Glu Gln Ala Val Leu Cys Gly Gly Leu Ser Ala Leu Val Lys Ala
        195                 200                 205

Gly Phe Glu Thr Leu Thr Glu Ala Gly Tyr Gln Pro Glu Leu Ala Tyr
    210                 215                 220

Phe Glu Cys Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Tyr Glu
225                 230                 235                 240

Glu Gly Leu Ala Gly Met Arg Tyr Ser Ile Ser Asp Thr Ala Gln Trp
                245                 250                 255

Gly Asp Phe Val Ser Gly Pro Arg Val Val Asp Ala Lys Val Lys Glu
            260                 265                 270

Ser Met Lys Glu Val Leu Lys Asp Ile Gln Asn Gly Thr Phe Ala Lys
        275                 280                 285

Glu Trp Ile Val Glu Asn Gln Val Asn Arg Pro Arg Phe Asn Ala Ile
    290                 295                 300

Asn Ala Ser Glu Asn Glu His Gln Ile Glu Val Val Gly Arg Lys Leu
305                 310                 315                 320

Arg Glu Met Met Pro Phe Val Lys Gln Gly Lys Lys Lys Glu Ala Val
                325                 330                 335

Val Ser Val Ala Gln Asn
            340
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[illegible]

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<211> 1674
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1674)

<400> 37
atg gca gaa tta cgc agt aat atg atc aca caa gga atc gat aga gct      48
Met Ala Glu Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala
  1               5                  10                  15

ccg cac cgc agt ttg ctt cgt gca gca ggg gta aaa gaa gag gat ttc      96
Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe
             20                  25                  30

ggc aag ccg ttt att gcg gtg tgt aat tca tac att gat atc gtt ccc     144
Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro
         35                  40                  45

ggt cat gtt cac ttg cag gag ttt ggg aaa atc gta aaa gaa gca atc     192
Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile
     50                  55                  60

aga gaa gca ggg ggc gtt ccg ttt gaa ttt aat acc att ggg gta gat     240
Arg Glu Ala Gly Gly Val Pro Phe Glu Phe Asn Thr Ile Gly Val Asp
 65                  70                  75                  80

gat ggc atc gca atg ggg cat atc ggt atg aga tat tcg ctg cca agc     288
Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser
                 85                  90                  95

cgt gaa att atc gca gat tct gtg gaa acg gtt gta tcc gca cat tgg     336
Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Val Ser Ala His Trp
            100                 105                 110

ttt gac gga atg gtc tgt att ccg aac tgc gac aaa atc aca ccg gga     384
Phe Asp Gly Met Val Cys Ile Pro Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125

atg ctt atg gcg gca atg cgc atc aac att ccg acg att ttt gtc agc     432
Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Phe Val Ser
    130                 135                 140

ggc gga ccg atg gcg gca gga aga aca agt tac ggg cga aaa atc tcc     480
Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser
145                 150                 155                 160

ctt tcc tca gta ttc gaa ggg gta ggc gcc tac caa gca ggc aaa atc     528
Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile
                165                 170                 175

aac gaa aac gag ctt caa gaa cta gag cag ttc gga tgc cca acg tgc     576
Asn Glu Asn Glu Leu Gln Glu Leu Glu Gln Phe Gly Cys Pro Thr Cys
            180                 185                 190

ggg tct tgc tca ggc atg ttt acg gcg aac tca atg aac tgc ctg tca     624
Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu Ser
        195                 200                 205
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gaa gca ctt ggt ctt gct ttg ccg ggt aat gga acc att ctg gca aca      672
Glu Ala Leu Gly Leu Ala Leu Pro Gly Asn Gly Thr Ile Leu Ala Thr
    210                 215                 220

tct ccg gaa cgc aaa gag ttt gtg aga aaa tcg gct gcg caa tta atg      720
Ser Pro Glu Arg Lys Glu Phe Val Arg Lys Ser Ala Ala Gln Leu Met
225                 230                 235                 240

gaa acg att cgc aaa gat atc aaa ccg cgt gat att gtt aca gta aaa      768
Glu Thr Ile Arg Lys Asp Ile Lys Pro Arg Asp Ile Val Thr Val Lys
                245                 250                 255

gcg att gat aac gcg ttt gca ctc gat atg gcg ctc gga ggt tct aca      816
Ala Ile Asp Asn Ala Phe Ala Leu Asp Met Ala Leu Gly Gly Ser Thr
            260                 265                 270

aat acc gtt ctt cat acc ctt gcc ctt gca aac gaa gcc ggc gtt gaa      864
Asn Thr Val Leu His Thr Leu Ala Leu Ala Asn Glu Ala Gly Val Glu
        275                 280                 285

tac tct tta gaa cgc att aac gaa gtc gct gag cgc gtg ccg cac ttg      912
Tyr Ser Leu Glu Arg Ile Asn Glu Val Ala Glu Arg Val Pro His Leu
    290                 295                 300

gct aag ctg gcg cct gca tcg gat gtg ttt att gaa gat ctt cac gaa      960
Ala Lys Leu Ala Pro Ala Ser Asp Val Phe Ile Glu Asp Leu His Glu
305                 310                 315                 320

gcg ggc ggc gtt tca gcg gct ctg aat gag ctt tcg aag aaa gaa gga     1008
Ala Gly Gly Val Ser Ala Ala Leu Asn Glu Leu Ser Lys Lys Glu Gly
                325                 330                 335

gcg ctt cat tta gat gcg ctg act gtt aca gga aaa act ctt gga gaa     1056
Ala Leu His Leu Asp Ala Leu Thr Val Thr Gly Lys Thr Leu Gly Glu
            340                 345                 350

acc att gcc gga cat gaa gta aag gat tat gac gtc att cac ccg ctg     1104
Thr Ile Ala Gly His Glu Val Lys Asp Tyr Asp Val Ile His Pro Leu
        355                 360                 365

gat caa cca ttc act gaa aag gga ggc ctt gct gtt tta ttc ggt aat     1152
Asp Gln Pro Phe Thr Glu Lys Gly Gly Leu Ala Val Leu Phe Gly Asn
    370                 375                 380

cta gct ccg gac ggc gct atc att aaa aca ggc ggc gta cag aat ggg     1200
Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly
385                 390                 395                 400

att aca aga cat gaa ggg ccg gct gtc gta ttc gat tct cag gac gag     1248
Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu
                405                 410                 415

gcg ctt gac ggc att atc aac cga aaa gta aaa gaa ggc gac gtt gtc     1296
Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val
            420                 425                 430

att att aga tat gaa ggg cca aaa ggc gga cct ggc atg ccg gaa atg     1344
Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met
        435                 440                 445

[illegible]
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Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
    450                 455                 460

gca ttg att acg gac gga cgt ttt tcc gga gcc tcc cgt ggc ctt tca     1440
Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
465                 470                 475                 480

atc ggc cac gta tca cct gag gcc gct gag ggc ggg ccg ctt gcc ttt     1488
Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe
                485                 490                 495

gtt gaa aac gga gac cat att atc gtt gat att gaa aaa cgc atc ttg     1536
Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu
            500                 505                 510

gat gta caa gtg cca gaa gaa gag tgg gaa aaa cga aaa gcg aac tgg     1584
Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp
        515                 520                 525

aaa ggt ttt gaa ccg aaa gtg aaa acc ggc tac ctg gca cgt tat tct     1632
Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
    530                 535                 540

aaa ctt gtg aca agt gcc aac acc ggc ggt att atg aaa atc             1674
Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
545                 550                 555


<210> 38
<211> 558
<212> PRT
<213> Bacillus subtilis

<400> 38
Met Ala Glu Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala
1               5                   10                  15

Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe
            20                  25                  30

Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro
        35                  40                  45

Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile
    50                  55                  60

Arg Glu Ala Gly Gly Val Pro Phe Glu Phe Asn Thr Ile Gly Val Asp
65                  70                  75                  80

Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser
                85                  90                  95

Arg Glu Ile Ile Ala Asp Ser Val Glu Thr Val Val Ser Ala His Trp
            100                 105                 110

Phe Asp Gly Met Val Cys Ile Pro Asn Cys Asp Lys Ile Thr Pro Gly
        115                 120                 125

Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Phe Val Ser
    130                 135                 140
```

```
Gly Gly Pro Met Ala Ala Gly Arg Thr Ser Tyr Gly Arg Lys Ile Ser
145                 150                 155                 160

Leu Ser Ser Val Phe Glu Gly Val Gly Ala Tyr Gln Ala Gly Lys Ile
                165                 170                 175

Asn Glu Asn Glu Leu Gln Glu Leu Glu Gln Phe Gly Cys Pro Thr Cys
            180                 185                 190

Gly Ser Cys Ser Gly Met Phe Thr Ala Asn Ser Met Asn Cys Leu Ser
        195                 200                 205

Glu Ala Leu Gly Leu Ala Leu Pro Gly Asn Gly Thr Ile Leu Ala Thr
    210                 215                 220

Ser Pro Glu Arg Lys Glu Phe Val Arg Lys Ser Ala Ala Gln Leu Met
225                 230                 235                 240

Glu Thr Ile Arg Lys Asp Ile Lys Pro Arg Asp Ile Val Thr Val Lys
                245                 250                 255

Ala Ile Asp Asn Ala Phe Ala Leu Asp Met Ala Leu Gly Gly Ser Thr
            260                 265                 270

Asn Thr Val Leu His Thr Leu Ala Leu Ala Asn Glu Ala Gly Val Glu
        275                 280                 285

Tyr Ser Leu Glu Arg Ile Asn Glu Val Ala Glu Arg Val Pro His Leu
    290                 295                 300

Ala Lys Leu Ala Pro Ala Ser Asp Val Phe Ile Glu Asp Leu His Glu
305                 310                 315                 320

Ala Gly Gly Val Ser Ala Ala Leu Asn Glu Leu Ser Lys Lys Glu Gly
                325                 330                 335

Ala Leu His Leu Asp Ala Leu Thr Val Thr Gly Lys Thr Leu Gly Glu
            340                 345                 350

Thr Ile Ala Gly His Glu Val Lys Asp Tyr Asp Val Ile His Pro Leu
        355                 360                 365

Asp Gln Pro Phe Thr Glu Lys Gly Gly Leu Ala Val Leu Phe Gly Asn
    370                 375                 380

Leu Ala Pro Asp Gly Ala Ile Ile Lys Thr Gly Gly Val Gln Asn Gly
385                 390                 395                 400

Ile Thr Arg His Glu Gly Pro Ala Val Val Phe Asp Ser Gln Asp Glu
                405                 410                 415

Ala Leu Asp Gly Ile Ile Asn Arg Lys Val Lys Glu Gly Asp Val Val
            420                 425                 430

Ile Ile Arg Tyr Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met
        435                 440                 445

Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
    450                 455                 460

Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
```

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465                 470                 475                 480

Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe
                485                 490                 495

Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu
            500                 505                 510

Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp
        515                 520                 525

Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
    530                 535                 540

Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
545                 550                 555


<210> 39
<211> 194
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
      sequence

<220>
<221> -35_signal
<222> (136)..(141)

<220>
<221> -10_signal
<222> (159)..(164)

<400> 39
gctattgacg acagctatgg ttcactgtcc accaaccaaa actgtgctca gtaccgccaa 60

tatttctccc ttgaggggta caaagaggtg tccctagaag agatccacgc tgtgtaaaaa 120

ttttacaaaa aggtattgac tttccctaca gggtgtgtaa taatttaatt acaggcgggg 180

gcaaccccgc ctgt                                                   194


<210> 40
<211> 163
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
      sequence

<220>
<221> -35_signal
<222> (113)..(118)

<220>
<221> -10_signal
<222> (136)..(141)
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<400> 40
gcctacctag cttccaagaa agatatccta acagcacaag agcggaaaga tgttttgttc 60

tacatccaga acaacctctg ctaaaattcc tgaaaaattt tgcaaaaagt tgttgacttt 120

atctacaagg tgtggtataa taatcttaac aacagcagga cgc 163

<210> 41
<211> 127
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
sequence

<220>
<221> -35_signal
<222> (34)..(39)

<220>
<221> -10_signal
<222> (58)..(63)

<220>
<221> -35_signal
<222> (75)..(80)

<220>
<221> -10_signal
<222> (98)..(103)

<400> 41
gaggaatcat agaattttgt caaaataatt ttattgacaa cgtcttatta acgttgatat 60

aatttaaatt ttatttgaca aaaatgggct cgtgttgtac aataaatgta gtgaggtgga 120

tgcaatg 127

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 42
taaacatgag gaggagaaaa catg 24

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome

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      binding site

<400> 43
attcgagaaa tggagagaat ataatatg                                        28

<210> 44
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 44
agaaaggagg tga                                                        13

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<220>
<221> misc_feature
<222> 17-20
<223> n = a, c, g, or t

<400> 45
ttaagaaagg aggtgannnn atg                                             23

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<220>
<221> misc_feature
<222> 16-20
<223> n = a, c, g, or t

<400> 46
ttagaaagga ggtgannnnn atg                                             23


<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site
```

```
<220>
<221> misc_feature
<222> 14-21
<223> n = a, c, g, or t

<400> 47
agaaaggagg tgannnnnnn atg                                                23

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<220>
<221> misc_feature
<222> 14-19
<223> n = a, c, g, or t

<400> 48
agaaaggagg tgannnnnna tg                                                 22

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 49
ccctttagaa ggaggagaaa acatg                                              25

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 50
ccctttagag gaggagaaaa catg                                               24

<210> 51
<211> [illegible]
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 51
[illegible]
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```
<210> 52
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 52
ttagaaagga ggtttaatta atg                                          23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 53
ttagaaagga ggtgatttaa atg                                          23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 54
ttagaaagga ggtgtttaaa atg                                          23

<210> 55
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 55
attcgagaaa ggaggtgaat ataatatg                                     28

<210> 56
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 56
[illegible]

<210> 57
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```
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
      binding site

<400> 57
attcgtagaa aggaggtgaa ttaatatg                                    26



<210> 58
<211> 3291
<212> DNA
<213> Bacillus subtilis

<400> 58
atggggacta atgtacaggt ggattcagca tctgccgaat gtacacagac gatgagcgga 60

gcattaatgc tgattgaatc attaaaaaaa gagaaagtag aaatgatctt cggttatccg 120

ggcggggctg tgcttccgat ttacgataag ctatacaatt cagggttggt acatatcctt 180

ccccgtcacg aacaaggagc aattcatgca gcggagggat acgcaagggt ctccggaaaa 240

ccgggtgtcg tcattgccac gtcagggccg ggagcgacaa accttgttac aggccttgct 300

gatgccatga ttgattcatt gccgttagtc gtctttacag ggcaggtagc aacctctgta 360

atcgggagcg atgcatttca ggaagcagac attttaggga ttacgatgcc agtaacaaaa 420

cacagctatt aggttcgcta gccggaagat ctgttgccga tcattaaaga agcgttccat 480

atttgaacaa ctggaagact cggacctgta ttgattgata ttccaaaaga tgtagcaaca 540

attgaaggag aattcagcta cgatcatgag atgaatctcc cgggatacca gccgacaaca 600

gagccgaatt atttgcagat ccgcaagctt gtggaagccg tgagcagtgc gaaaaaaccg 660

gtgatcctgg cgggtgcggg cgtactgcac ggaaaacggt cagaagaatt aaaaaattat 720

gctgaacagc agcaaatccc tgtggcacac accctttggg ggctcggagg cttcccggct 780

gacaatccgc ttttcctagg gatggcggga atgcacggta cttatacagc caatatggtt 840

cttcatgaat gtgatctatt aattagtatc ggcgcccgtt ttgatgacgg tgttacagga 900

aacctgaaac actttgccag aaacgcaaag atatcccaca tcgatattga tctcactgaa 960

atccaaaaaa tcatgaaaat [illegible] [illegible] [illegible] [illegible] 1020

[illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 1080

[illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 1140

[illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 1200

[illegible] [illegible] [illegible] [illegible] [illegible] [illegible] 1260
```

gtcacgtcag gcggacttgg aacgatggga ttcggtcttc cggcggcgat cggcgcacag 1320

ctggccgaaa aagatgctac tgttgtcgcg gttgtcggag acggcggatt ccaaatgacg 1380

cttcaagaac tcgatgttat tcgcgaatta aatcttccgg ttaaggtagt gattttaaat 1440

aacgcttgtc tcggaatggt cagacagtgg caggaaattt tctatgaaga acgttattca 1500

gaatctaaat tcgcttctca gcctgacttc gtcaaattgt ccgaagcata cggcattaaa 1560

ggcatcagaa tttcatcaga agcggaagca aaggaaaagc tggaagaggc attaacatca 1620

agagaacctg ttgtcattga cgtgcgggtt gccagcgaag aaaaagtatt cccgatggtg 1680

gctccgggga aagggctgca tgaaatggtg gggtgaaac cttgaaaaga attatcacat 1740

tgactgtggt gaaccgctcc ggggtgttaa accggatcac cggtctattc acaaaaaggc 1800

attacaacat tgaaagcatt acagttggac acacagaaac agccggcgtt tccagaatca 1860

ccttcgtcgt tcatgttgaa ggtgaaaatg atgttgaaca gttaacgaaa cagctcaaca 1920

aacagattga tgtgctgaaa gtcacagaca tcacaaatca atcgattgtc cagagggagc 1980

tggccttaat caaggttgtc tccgcacctt caacaagaac agagattaat ggaatcatag 2040

aacggtttag agcctctgtc gttgatgtca gcagagacag catcgttgtt caggtgacag 2100

gtgaatctaa caaaattgaa gcgcttattg agttattaaa accttatggc attaaagaaa 2160

tcgcgagaac aggtacaacg gcttttgcga ggggaaccag caaaaggcgt catccaataa 2220

aacaatatct attgtataaa acataacaag ggagagattg aaatggtaaa actatattat 2280

aacggcgata tcaaagagaa cgtattggct ggaaaaacag tagcggctat ccggtacggt 2340

tcgtaaggcc acgcacatgc cctgaacctt aaagaaagcg gagtagacgt gatcgtcggt 2400

gttagacaag gaaaatcttt cactcaagcc caagaagacg gacataaagt attttcagta 2460

aaagaagcgg cagcccaagc cgaaatcatc atggttctgc ttccggatga gcagcagcaa 2520

aaactatacg aagctgaaat caaagatgaa ttgacagcag gaaaatcatt agtattcgct 2580

catggattta acgtgcattt ccatcaaatt gttcctccgg cggatgtaga tgtattctta 2640

gtggcccctа aaggcccggg acaattggta aagaagacat atcagcaacg agctggcgta 2700

cctgcattgt tcgcaatcta tcaagatgtg actggagaag caagacacaa agcgctcgct 2760

tatgctaaag gaatcggcgg cgcaaagacg agcgtattac aaacgacatt taaagaagaa 2820

acagaaacag atttgctcgg tgagcaagca gttctttgcg gcggattaac cgcgcttatc 2880

aaagcgggat ttgaaactct aacgaacgca [illegible] 2940

[illegible]

[illegible]

[illegible]

```
gcaaaagagt ggatcgtcga aaaccaagta aaccgtcctc gtttcaacgc tatcaatgca 3180

agcgagaacg aacatcaaat cgaagtagtg ggaagaaagc ttcgtgaaat gatgccgttt 3240

gtgaaacaag gcaagaagaa ggaagcggtg gtctccgttg cgcaaaatta a          3291


<210> 59
<211> 2363
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (242)..(1072)

<220>
<221> CDS
<222> (1077)..(1934)

<220>
<221> CDS
<222> (1939)..(2319)

<400> 59
ttggtacaag cccgttgatt ttggtatact tccattgggc agtatcgcct gcgaactgca 60

cctattatta aaatagatag acattgcagc agtctgcctt gatccaaaaa aggactggga 120

cagagggatg aaactcgccg aactttagaa agtgaagaat cctctcgtt gtaacggaag 180

gtttttttgc ttgcagaaga aaacggcaga tcatctcctc taaacatgag gaggagaaaa 240

c atg aaa aca aaa ctg gat ttt cta aaa atg aag gag tct gaa gaa ccg 289
  Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
  1               5                   10                  15

att gtc atg ctg acc gct tat gat tat ccg gca gct aaa ctt gct gaa   337
Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
            20                  25                  30

caa gcg gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc   385
Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
        35                  40                  45

gtt ctc ggc ctt gat tca act gtc ggt gtg aca gtt gcg gac atg att   433
Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
    50                  55                  60

cat cat acg aaa gcc gtt aaa agg ggt gcg ccg aat acc ttt att gtg   481
His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
65                  70                  75                  80

aca gat atg ccg ttt atg tct tat cac ctg tct aag gaa gat acg ctg   529
Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
                85                  90                  95

aaa aat gca gcg gct atc gtt cag gaa agc ggc gct gat gca ctg aag   577
Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys
            100                 105                 110
```

```
ctt gag ggt gga gaa ggc gtg ttt gaa tcc att cgc gca ttg acg ctt     625
Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu
        115                 120                 125

gga ggc att cca gta gtc agt cat tta ggt ttg aca ccg cag tca gtc     673
Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val
    130                 135                 140

ggc gta ctg ggc ggc tat aaa gta cag ggc aaa gac gaa caa agc gcc     721
Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala
145                 150                 155                 160

aaa aaa tta ata gaa gac agt ata aaa tgc gaa gaa gca gga gct atg     769
Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met
                165                 170                 175

atg ctt gtg ctg gaa tgt gtg ccg gca gaa ctc aca gcc aaa att gcc     817
Met Leu Val Leu Glu Cys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala
            180                 185                 190

gag acg cta agc ata ccg gtc att gga atc ggg gct ggt gtg aaa gcg     865
Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala
        195                 200                 205

gac gga caa gtt ctc gtt tat cat gat att atc ggc cac ggt gtt gag     913
Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Glu
    210                 215                 220

aga aca cct aaa ttt gta aag caa tat acg cgc att gat gaa acc atc     961
Arg Thr Pro Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile
225                 230                 235                 240

gaa aca gca atc agc gga tat gtt cag gat gta aga cat cgt gct ttc     1009
Glu Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Phe
                245                 250                 255

cct gaa caa aag cat tcc ttt caa atg aac cag aca gtg ctt gac ggc     1057
Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
            260                 265                 270

ttg tac ggg gga aaa taag atg aga cag att act gat att tca cag ctg    1106
Leu Tyr Gly Gly Lys      Met Arg Gln Ile Thr Asp Ile Ser Gln Leu
        275                     280                 285

aaa gaa gcc ata aaa caa tac cat tca gag ggc aag tca att gga ttt     1154
Lys Glu Ala Ile Lys Gln Tyr His Ser Glu Gly Lys Ser Ile Gly Phe
        290                 295                 300

gtt ccg acg atg ggg ttt ctg cat gag ggg cat tta act tta gca gat     1202
Val Pro Thr Met Gly Phe Leu His Glu Gly His Leu Thr Leu Ala Asp
    305                 310                 315

aaa gca aga caa gaa aat gat gcc gtt att atg agt att ttt gtt aat     1250
Lys Ala Arg Gln Glu Asn Asp Ala Val Ile Met Ser Ile Phe Val Asn
320                 325                 330                 335

cct gca caa ttc ggc cct aat caa gat ttt caa gca tat cct cgt gat     1298
Pro Ala Gln Phe Gly Pro Asn Gln Asp Phe Gln Ala Tyr Pro Arg Asp
                340                 345                 350
```

```
att gag cgg gat gca gct ctt gca gaa aac gcc gga gtc gat att ctt     1346
Ile Glu Arg Asp Ala Ala Leu Ala Glu Asn Ala Gly Val Asp Ile Leu
            355                 360                 365

ttt acg cca gat gct cat gat atg tat ccc ggt gaa aag aat gtc acg     1394
Phe Thr Pro Asp Ala His Asp Met Tyr Pro Gly Glu Lys Asn Val Thr
        370                 375                 380

att cat gta gaa aga cgc aca gac gtg tta tgc ggg cgc tca aga gaa     1442
Ile His Val Glu Arg Arg Thr Asp Val Leu Cys Gly Arg Ser Arg Glu
    385                 390                 395

gga cat ttt gac ggg gtc gcg atc gta ctg acg aag ctt ttc aat cta     1490
Gly His Phe Asp Gly Val Ala Ile Val Leu Thr Lys Leu Phe Asn Leu
400                 405                 410                 415

gtc aag ccg act cgt gcc tat ttc ggt tta aaa gat gcg cag cag gta     1538
Val Lys Pro Thr Arg Ala Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val
                420                 425                 430

gct gtt gtt gat ggg tta atc agc gac ttc ttc atg gat att gaa ttg     1586
Ala Val Val Asp Gly Leu Ile Ser Asp Phe Phe Met Asp Ile Glu Leu
            435                 440                 445

gtt cct gtc gat acg gtc aga gag gaa gac ggc tta gcc aaa agc tct     1634
Val Pro Val Asp Thr Val Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser
        450                 455                 460

cgc aat gta tac tta aca gct gag gaa aga aaa gaa gcg cct aag ctg     1682
Arg Asn Val Tyr Leu Thr Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu
    465                 470                 475

tat cgg gct ctt caa aca agt gcg gaa ctt gtt caa gcc ggt gaa aga     1730
Tyr Arg Ala Leu Gln Thr Ser Ala Glu Leu Val Gln Ala Gly Glu Arg
480                 485                 490                 495

gat cct gaa gcg gtg ata aaa gct gca aaa gat atc att gaa acg act     1778
Asp Pro Glu Ala Val Ile Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr
                500                 505                 510

agc gga acc ata gac tat gta gag ctt tat tcc tat ccg gaa ctt gag     1826
Ser Gly Thr Ile Asp Tyr Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu
            515                 520                 525

cct gtg aat gaa att gct gga aag atg att ctt gct gtt gca gtt gct     1874
Pro Val Asn Glu Ile Ala Gly Lys Met Ile Leu Ala Val Ala Val Ala
        530                 535                 540

ttt tca aaa gcg cgt tta ata gat aat atc att att gat att cga gaa     1922
Phe Ser Lys Ala Arg Leu Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu
    545                 550                 555

atg gag aga ata taat atg tat cga aca atg atg agc ggt aaa ctt cat    [illegible]
Met Glu Arg Ile      Met Tyr Arg Thr Met Met Ser Gly Lys Leu His
560                      5                   10

[illegible]
Arg Ala Thr Val Thr Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr
15                  20                  25                  30

[illegible]
```

```
Ile Asp Glu Asp Leu Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys
                595                 600                 605

gta caa att gtg aat aat aat aat gga gca cgt ctt gaa acg tat att     2115
Val Gln Ile Val Asn Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile
            610                 615                 620

att cct ggt aaa cgg gga agc ggc gtc ata tgc tta aac ggt gca gcc     2163
Ile Pro Gly Lys Arg Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala
        625                 630                 635

gca cgc ctt gtg cag gaa gga gat aag gtc att att att tcc tac aaa     2211
Ala Arg Leu Val Gln Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys
    640                 645                 650

atg atg tct gat caa gaa gcg gca agc cat gag ccg aaa gtg gct gtt     2259
Met Met Ser Asp Gln Glu Ala Ala Ser His Glu Pro Lys Val Ala Val
655                 660                 665                 670

ctg aat gat caa aac aaa att gaa caa atg ctg ggg aac gaa cca gcc     2307
Leu Asn Asp Gln Asn Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala
                675                 680                 685

cgt aca att ttg tagaagaaaa gccccctta tcgggggttt tcttttaaga tttt     2363
Arg Thr Ile Leu
            690


<210> 60
<211> 293
<212> PRT
<213> Bacillus subtilis

<400> 60
Met Ser Ile Ala Val Ser Glu Glu Glu Ala Lys Ala Val Glu Gly Leu
1               5                   10                  15

Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu
            20                  25                  30

Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
        35                  40                  45

His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
    50                  55                  60

Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
65                  70                  75                  80

Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
                85                  90                  95

Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
            100                 105                 110

Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Thr Ser Tyr Asp Val
        115                 120                 125

Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
    130                 135                 140
```

```
Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
145                 150                 155                 160

Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
                165                 170                 175

Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
            180                 185                 190

Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu
        195                 200                 205

Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
    210                 215                 220

Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
225                 230                 235                 240

Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
                245                 250                 255

Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
            260                 265                 270

Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
        275                 280                 285

Leu Val Arg Arg Val
    290


<210> 61
<211> 281
<212> PRT
<213> Bacillus subtilis

<400> 61
Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile
  1               5                  10                  15

Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala
             20                  25                  30

Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
         35                  40                  45

Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
     50                  55                  60

Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
 65                  70                  75                  80

Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr
                 85                  90                  95

Ala Gln Leu Lys Lys Lys Asn Met Met Ser Arg Lys Gly Ile Pro Glu
            100                 105                 110

Ser Tyr Asp Val Lys Ala Leu Leu Gln Phe Leu Asn Asp Leu Lys Ser
        115                 120                 125
```

```
Gly Lys Asp Ser Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp
    130                 135                 140

Arg Glu Glu Gly Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile
145                 150                 155                 160

Ile Glu Gly Ile Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg
                165                 170                 175

Glu Asn Pro Arg Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr
            180                 185                 190

Val Asp Ala Glu Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe
        195                 200                 205

Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His
    210                 215                 220

Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser
225                 230                 235                 240

Ile Trp Glu Ser Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro
                245                 250                 255

Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys
            260                 265                 270

Val Glu Glu Val Leu Val Arg Arg Val
        275                 280


<210> 62
<211> 1092
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1089)

<400> 62
atg act aaa caa aca att cgc gtt gaa ttg aca tca aca aaa aaa ccg      48
Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
  1               5                  10                  15

aaa cca gac cca aat cag ctt tcg ttc gga aga gtg ttt aca gac cac      96
Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
            20                  25                  30

atg ttt gta atg gac tat gcc gca gat aaa ggt tgg tac gat cca aga     144
Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
        35                  40                  45

atc att cct tat caa ccc tta tca atg gat cca act gca atg gtt tat     192
Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
    50                  55                  60

cat tac ggt caa acc gtg ttt gaa ggg tta aag gct tac gtg tca gag     240
His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
65                  70                  75                  80
```

```
gat gac cat gtt ctg ctt ttc aga ccg gaa aaa aat atg gaa cgc ctg    288
Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
                 85                  90                  95

aat caa tca aac gac cgc ctc tgc atc ccg caa att gat gaa gaa cag    336
Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
            100                 105                 110

gtt ctt gaa ggc tta aag cag ctt gtc gca att gat aaa gac tgg att    384
Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
        115                 120                 125

cca aat gcg gag ggc acg tcc ctt tac atc cgt ccg ttc atc atc gca    432
Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
    130                 135                 140

acc gag cct ttc ctt ggt gtt gcg gca tct cat acg tat aag ctc ttg    480
Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
145                 150                 155                 160

atc att ctt tct ccg gtc ggc tct tat tac aaa gaa ggc att aag ccg    528
Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro
                165                 170                 175

gtc aaa atc gct gtt gaa agt gaa ttt gtc cgt gcg gta aaa ggc gga    576
Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly
            180                 185                 190

aca gga aat gcc aaa acc gca gga aac tat gct tca agc tta aaa gcg    624
Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala
        195                 200                 205

cag cag gta gcc gaa gag aaa gga ttt tct caa gta ctc tgg ctc gac    672
Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp
    210                 215                 220

ggc att gag aag aaa tac atc gaa gaa gtc gga agc atg aac atc ttc    720
Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe
225                 230                 235                 240

ttc aaa atc aac ggt gaa atc gta aca ccg atg ctg aac ggc agc atc    768
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile
                245                 250                 255

ctg gaa ggc att acg cgc aat tca gtc atc gcc ttg ctt aag cat tgg    816
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp
            260                 265                 270

ggc ctt caa gtt tca gaa cga aaa att gcg atc gat gag gtc atc caa    864
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln
        275                 280                 285

gcc cat aaa gat ggc atc ctg gaa gaa gcc ttc gga aca ggt aca gca    912
Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala
    290                 295                 300

gct gtt att tct cca gtc ggc gag ctg att tgg cag gat gaa aca ctt    960
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu
305                 310                 315                 320

[illegible]
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```
Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp
                325                 330                 335

acg att aca ggc att caa aaa ggc gct gtc gca gac gaa ttc gga tgg     1056
Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp
            340                 345                 350

acg acc gaa gtc gca gcg ctg act gaa agc aag taa                     1092
Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
        355                 360


<210> 63
<211> 363
<212> PRT
<213> Bacillus subtilis

<400> 63
Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
  1               5                  10                  15

Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
            20                  25                  30

Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
        35                  40                  45

Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
    50                  55                  60

His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
 65                  70                  75                  80

Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
                 85                  90                  95

Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
            100                 105                 110

Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
        115                 120                 125

Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
    130                 135                 140

Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
145                 150                 155                 160

Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro
                165                 170                 175

Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly
            180                 185                 190

Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala
        195                 200                 205

Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp
    210                 215                 220

Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe
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225                 230                 235                 240

Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile
                245                 250                 255

Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp
            260                 265                 270

Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln
        275                 280                 285

Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala
    290                 295                 300

Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu
305                 310                 315                 320

Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp
                325                 330                 335

Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp
            340                 345                 350

Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
        355                 360


<210> 64
<211> 1071
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1068)

<400> 64
ttg aat aag ctt att gaa cga gaa aaa act gta tat tat aag gaa aag      48
Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys
  1               5                  10                  15

ccc gac ccg tct tcc ttg ggg ttt gga caa tat ttt aca gat tat atg      96
Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met
            20                  25                  30

ttt gtg atg gac tac gaa gag ggg att gga tgg cat cat ccg aga att     144
Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile
        35                  40                  45

gcg ccg tac gca ccg ctt acg ctt gat ccg tct tca tct gtt ttt cat     192
Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His
    50                  55                  60

tac ggc cag gct gtt ttt gaa gga tta aaa gca tac aga aca gac gac     240
Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp
65                  70                  75                  80

[illegible] agg gtg [illegible] [illegible] ttt cgt [illegible] gat caa aat att aaa [illegible] [illegible] aat     288
Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn
                85                  90                  95
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```
aga tcg tgt gag cgc atg agc atg ccc cct tta gac gaa gag ctg gtg     336
Arg Ser Cys Glu Arg Met Ser Met Pro Pro Leu Asp Glu Glu Leu Val
            100                 105                 110

ctt gag gca ttg acg caa tta gtt gag ctg gag aaa gat tgg gtt cca     384
Leu Glu Ala Leu Thr Gln Leu Val Glu Leu Glu Lys Asp Trp Val Pro
        115                 120                 125

aag gaa aaa gga acg tca ctg tat att cgt cct ttt gtc att gcc aca     432
Lys Glu Lys Gly Thr Ser Leu Tyr Ile Arg Pro Phe Val Ile Ala Thr
    130                 135                 140

gaa ccg agt ctc ggt gtg aag gca tcc agg agc tat aca ttt atg atc     480
Glu Pro Ser Leu Gly Val Lys Ala Ser Arg Ser Tyr Thr Phe Met Ile
145                 150                 155                 160

gtg ctt tcg cct gtc ggc tcc tat tat ggc gac gat cag ctg aag ccg     528
Val Leu Ser Pro Val Gly Ser Tyr Tyr Gly Asp Asp Gln Leu Lys Pro
                165                 170                 175

gtt aga atc tat gtc gaa gat gag tat gtg agg gcg gtc aac gga gga     576
Val Arg Ile Tyr Val Glu Asp Glu Tyr Val Arg Ala Val Asn Gly Gly
            180                 185                 190

gtc ggg ttt gca aaa acg gct gga aac tat gcc gcc agt ctt cag gca     624
Val Gly Phe Ala Lys Thr Ala Gly Asn Tyr Ala Ala Ser Leu Gln Ala
        195                 200                 205

cag cgg aaa gcg aat gaa ctg ggc tat gac cag gta ctg tgg ctg gac     672
Gln Arg Lys Ala Asn Glu Leu Gly Tyr Asp Gln Val Leu Trp Leu Asp
    210                 215                 220

gcc atc gaa aag aaa tat gtg gaa gaa gta ggg agc atg aac atc ttt     720
Ala Ile Glu Lys Lys Tyr Val Glu Glu Val Gly Ser Met Asn Ile Phe
225                 230                 235                 240

ttc gtc ata aac ggg gaa gct gtc aca cct gct tta agc gga agc att     768
Phe Val Ile Asn Gly Glu Ala Val Thr Pro Ala Leu Ser Gly Ser Ile
                245                 250                 255

tta agc ggg gtt aca cgt gcg tct gcg att gaa ttg att cga agc tgg     816
Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp
            260                 265                 270

ggc att ccg gtt cgt gaa gag aga ata tcg att gat gag gtg tat gcg     864
Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala
        275                 280                 285

gcc tct gca cgc gga gaa ttg aca gag gtc ttt ggc aca ggc acg gca     912
Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala
    290                 295                 300

gca gtc gtt acg cct gtc ggt gaa ctc aac att cat gga aaa acg gtg     960
Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val
305                 310                 315                 320

[illegible]
Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu
                325                 330                 335

[illegible]
```

```
Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
            340                 345                 350

aca gtg gaa gtg tga                                                 1071
Thr Val Glu Val
        355


<210> 65
<211> 356
<212> PRT
<213> Bacillus subtilis

<400> 65
Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys
1               5                   10                  15

Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met
            20                  25                  30

Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile
        35                  40                  45

Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His
    50                  55                  60

Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp
65                  70                  75                  80

Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn
                85                  90                  95

Arg Ser Cys Glu Arg Met Ser Met Pro Pro Leu Asp Glu Glu Leu Val
            100                 105                 110

Leu Glu Ala Leu Thr Gln Leu Val Glu Leu Glu Lys Asp Trp Val Pro
        115                 120                 125

Lys Glu Lys Gly Thr Ser Leu Tyr Ile Arg Pro Phe Val Ile Ala Thr
    130                 135                 140

Glu Pro Ser Leu Gly Val Lys Ala Ser Arg Ser Tyr Thr Phe Met Ile
145                 150                 155                 160

Val Leu Ser Pro Val Gly Ser Tyr Tyr Gly Asp Asp Gln Leu Lys Pro
                165                 170                 175

Val Arg Ile Tyr Val Glu Asp Glu Tyr Val Arg Ala Val Asn Gly Gly
            180                 185                 190

Val Gly Phe Ala Lys Thr Ala Gly Asn Tyr Ala Ala Ser Leu Gln Ala
        195                 200                 205

Gln Arg Lys Ala Asn Glu Leu Gly Tyr Asp Gln Val Leu Trp Leu Asp
    210                 215                 220

Ala Ile Glu Lys Lys Tyr Val Glu Glu Val Gly Ser Met Asn Ile Phe
225                 230                 235                 240

Phe Val Ile Asn Gly Glu Ala Val Thr Pro Ala Leu Ser Gly Ser Ile
                245                 250                 255
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```
Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp
            260                 265                 270

Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala
        275                 280                 285

Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala
    290                 295                 300

Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val
305                 310                 315                 320

Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu
                325                 330                 335

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
            340                 345                 350

Thr Val Glu Val
        355


<210> 66
<211> 1428
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1425)

<400> 66
atg tta aac ggc caa aaa gaa tat cgc gtg gaa aaa gac ttc ctt ggc      48
Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
1               5                   10                  15

gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt      96
Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
            20                  25                  30

gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg      144
Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
        35                  40                  45

att aac gca ctg gcg att gtg aaa aaa gct gca gct ctt gcc aac atg      192
Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
    50                  55                  60

gac gtg aaa cgg ctg tat gaa gga att ggc caa gct atc gta caa gct      240
Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
65                  70                  75                  80

gct [illegible] [illegible] att ctg gaa ggc [illegible] tgg [illegible] gat [illegible] ttt atc [illegible] [illegible]      288
Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp
                85                  90                  95

tgg att caa [illegible] ggt [illegible] gga act [illegible] atg aat atg aac [illegible] aat [illegible]      336
Trp Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu
            100                 105                 110
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gtt atc gga aac cgg gcg ctt gaa atc atg gga cat aaa aag gga gat     384
Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp
        115                 120                 125

tat atc cat tta agt cca aac aca cat gtg aac atg tca cag tct cag     432
Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln
    130                 135                 140

aac gat gtg ttc ccg act gct atc cat att tcc aca ttg aag ctc tta     480
Asn Asp Val Phe Pro Thr Ala Ile His Ile Ser Thr Leu Lys Leu Leu
145                 150                 155                 160

gaa aaa ctg ctg aaa aca atg gaa gat atg cat agt gtg ttt aaa caa     528
Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln
                165                 170                 175

aaa gca cag gag ttt cac tct gtt att aaa atg ggc cgg aca cac ctt     576
Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu
            180                 185                 190

caa gat gcg gtt ccg atc cgt ctt ggc cag gaa ttc gaa gct tac agc     624
Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser
        195                 200                 205

cgt gtt ctc gag cgt gat atc aaa cga atc aag caa tcg cgc cag cac     672
Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His
    210                 215                 220

ctg tat gaa gtc aac atg ggc gca act gct gtt ggt aca ggg ctg aac     720
Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn
225                 230                 235                 240

gct gat cct gaa tat atc aaa cag gta gta aag cac ctt gct gat att     768
Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile
                245                 250                 255

agc ggg ctt cct ctt gtc ggc gct gat cat ctt gtt gat gcg aca caa     816
Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln
            260                 265                 270

aat aca gat gcc tat aca gag gta tca gct tca tta aaa gtc tgc atg     864
Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met
        275                 280                 285

atg aac atg tcg aag atc gca aac gac ctg cgc tta atg gcg tcg gga     912
Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly
    290                 295                 300

ccg cgc gcc gga ctt gcg gaa att tct ctg cct gca cgt cag ccg ggt     960
Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly
305                 310                 315                 320

tca tct att atg ccg ggg aaa gtc aat ccg gtt atg gcg gag ctg atc     1008
Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile
                325                 330                 335

aac caa att gcc ttc cag gtt att gga aat gat aat aca att tgt ctt     1056
Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu
            340                 345                 350

[illegible]                                                         1104
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Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu
        355                 360                 365

gtc ttt aat ttg ctt caa tcc atc agc atc atg aac aac ggc ttc cgt     1152
Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg
    370                 375                 380

tcg ttc act gac aac tgc tta aaa ggc att gaa gcc aat gaa aag cgt     1200
Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg
385                 390                 395                 400

atg aag caa tac gta gaa aaa agc gca ggc gtg atc aca gct gtc aat     1248
Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn
                405                 410                 415

ccg cat ctt ggg tat gaa gcg gca gct aga att gcc agg gaa gca att     1296
Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile
            420                 425                 430

atg aca ggg caa tct gtc cgg gat ctt tgt ctg cag cat gat gtg ctg     1344
Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu
        435                 440                 445

act gaa gaa gaa ttg gat att att tta aac cca tat gag atg acc aaa     1392
Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
    450                 455                 460

cca ggt atc gca ggg aaa gaa cta tta gaa aaa taa                     1428
Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
465                 470                 475


<210> 67
<211> 475
<212> PRT
<213> Bacillus subtilis

<400> 67
Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
  1               5                  10                  15

Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
            20                  25                  30

Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
        35                  40                  45

Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
    50                  55                  60

Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
65                  70                  75                  80

Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp
                85                  90                  95

Trp Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Glu
            100                 105                 110

Val Ile Gly Asn Arg Ala Leu Glu Ile Met Gly His Lys Lys Gly Asp
        115                 120                 125
```

```
Tyr Ile His Leu Ser Pro Asn Thr His Val Asn Met Ser Gln Ser Gln
    130                 135                 140

Asn Asp Val Phe Pro Thr Ala Ile His Ile Ser Thr Leu Lys Leu Leu
145                 150                 155                 160

Glu Lys Leu Leu Lys Thr Met Glu Asp Met His Ser Val Phe Lys Gln
                165                 170                 175

Lys Ala Gln Glu Phe His Ser Val Ile Lys Met Gly Arg Thr His Leu
            180                 185                 190

Gln Asp Ala Val Pro Ile Arg Leu Gly Gln Glu Phe Glu Ala Tyr Ser
        195                 200                 205

Arg Val Leu Glu Arg Asp Ile Lys Arg Ile Lys Gln Ser Arg Gln His
    210                 215                 220

Leu Tyr Glu Val Asn Met Gly Ala Thr Ala Val Gly Thr Gly Leu Asn
225                 230                 235                 240

Ala Asp Pro Glu Tyr Ile Lys Gln Val Val Lys His Leu Ala Asp Ile
                245                 250                 255

Ser Gly Leu Pro Leu Val Gly Ala Asp His Leu Val Asp Ala Thr Gln
            260                 265                 270

Asn Thr Asp Ala Tyr Thr Glu Val Ser Ala Ser Leu Lys Val Cys Met
        275                 280                 285

Met Asn Met Ser Lys Ile Ala Asn Asp Leu Arg Leu Met Ala Ser Gly
    290                 295                 300

Pro Arg Ala Gly Leu Ala Glu Ile Ser Leu Pro Ala Arg Gln Pro Gly
305                 310                 315                 320

Ser Ser Ile Met Pro Gly Lys Val Asn Pro Val Met Ala Glu Leu Ile
                325                 330                 335

Asn Gln Ile Ala Phe Gln Val Ile Gly Asn Asp Asn Thr Ile Cys Leu
            340                 345                 350

Ala Ser Glu Ala Gly Gln Leu Glu Leu Asn Val Met Glu Pro Val Leu
        355                 360                 365

Val Phe Asn Leu Leu Gln Ser Ile Ser Ile Met Asn Asn Gly Phe Arg
    370                 375                 380

Ser Phe Thr Asp Asn Cys Leu Lys Gly Ile Glu Ala Asn Glu Lys Arg
385                 390                 395                 400

Met Lys Gln Tyr Val Glu Lys Ser Ala Gly Val Ile Thr Ala Val Asn
                405                 410                 415

Pro His Leu Gly Tyr Glu Ala Ala Ala Arg Ile Ala Arg Glu Ala Ile
            420                 425                 430

Met Thr Gly Gln Ser Val Arg Asp Leu Cys Leu Gln His Asp Val Leu
        435                 440                 445
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Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
    450                 455                 460

Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
465                 470                 475


<210> 68
<211> 768
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(765)

<400> 68
atg aaa cga gaa agc aac att caa gtg ctc agc cgt ggt caa aaa gat      48
Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
  1               5                  10                  15

cag cct gtg agc cag att tat caa gta tca aca atg act tct cta tta      96
Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
             20                  25                  30

gac gga gta tat gac gga gat ttt gaa ctg tca gag att ccg aaa tat     144
Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
         35                  40                  45

gga gac ttc ggt atc gga acc ttt aac aag ctt gac gga gag ctg att     192
Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
     50                  55                  60

ggg ttt gac ggc gaa ttt tac cgt ctt cgc tca gac gga acc gcg aca     240
Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
 65                  70                  75                  80

ccg gtc caa aat gga gac cgt tca ccg ttc tgt tca ttt acg ttc ttt     288
Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
                 85                  90                  95

aca ccg gac atg acg cac aaa att gat gcg aaa atg aca cgc gaa gac     336
Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
            100                 105                 110

ttt gaa aaa gag atc aac agc atg ctg cca agc aga aat tta ttt tat     384
Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
        115                 120                 125

gca att cgc att gac gga ttg ttt aaa aag gtg cag aca aga aca gta     432
Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
    130                 135                 140

gaa ctt caa gaa aaa cct tac gtg cca atg gtt gaa gcg gtg aaa aca     480
Glu Leu Gln Glu Lys Pro Tyr Val Pro Met Val Glu Ala Val Lys Thr
145                 150                 155                 160

cag ccg att ttc aat ttc gat aat gtg aga gga acg att gta ggc ttt     528
Gln Pro Ile Phe Asn Phe Asp Asn Val Arg Gly Thr Ile Val Gly Phe
                165                 170                 175
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ttg aca cca gct tat gca aac gga atc gcc gtt tct ggc tat cac ctg      576
Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu
            180                 185                 190

cac ttc att gac gaa gga cgc aat tca ggc gga cac gtt ttt gac tat      624
His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
        195                 200                 205

gtg ctt gag gat tgc acg gtt acg att tct caa aaa atg aac atg aat      672
Val Leu Glu Asp Cys Thr Val Thr Ile Ser Gln Lys Met Asn Met Asn
    210                 215                 220

ctc aga ctt ccg aac aca gcg gat ttc ttt aat gcg aat ctg gat aac      720
Leu Arg Leu Pro Asn Thr Ala Asp Phe Phe Asn Ala Asn Leu Asp Asn
225                 230                 235                 240

cct gat ttt gcg aaa gat atc gaa aca act gaa gga agc cct gaa taa      768
Pro Asp Phe Ala Lys Asp Ile Glu Thr Thr Glu Gly Ser Pro Glu
                245                 250                 255


<210> 69
<211> 255
<212> PRT
<213> Bacillus subtilis

<400> 69
Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
  1               5                  10                  15

Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
             20                  25                  30

Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
         35                  40                  45

Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
     50                  55                  60

Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
 65                  70                  75                  80

Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
                 85                  90                  95

Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
            100                 105                 110

Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
        115                 120                 125

Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
    130                 135                 140

Glu Leu Gln Glu Lys Pro Tyr Val Pro Met Val Glu Ala Val Lys Thr
145                 150                 155                 160

Gln Pro Ile Phe Asn Phe Asp Asn Val Arg Gly Thr Ile Val Gly Phe
                165                 170                 175

Leu Thr Pro Ala Tyr Ala Asn Gly Ile Ala Val Ser Gly Tyr His Leu
```

```
                180                 185                 190

His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
        195                 200                 205

Val Leu Glu Asp Cys Thr Val Thr Ile Ser Gln Lys Met Asn Met Asn
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Leu Arg Leu Pro Asn Thr Ala Asp Phe Phe Asn Ala Asn Leu Asp Asn
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Pro Asp Phe Ala Lys Asp Ile Glu Thr Thr Glu Gly Ser Pro Glu
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acg ctg ttg atg gaa gat ctg aac gac ggt tta cgc acg cct ggc gcg      96
Thr Leu Leu Met Glu Asp Leu Asn Asp Gly Leu Arg Thr Pro Gly Ala
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att atg ctc ggc ggc ggt aat ccg gcg cag atc ccg gaa atg cag gac     144
Ile Met Leu Gly Gly Gly Asn Pro Ala Gln Ile Pro Glu Met Gln Asp
        35                  40                  45

tac ttc cag acg cta ctg acc gac atg ctg gaa agt ggc aaa gcg act     192
Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr
    50                  55                  60

gat gca ctg tgt aac tac gac ggt cca cag ggg aaa acg gag cta ctc     240
Asp Ala Leu Cys Asn Tyr Asp Gly Pro Gln Gly Lys Thr Glu Leu Leu
 65                  70                  75                  80

aca ctg ctt gcc gga atg ctg cgc gag aag ttg ggt tgg gat atc gaa     288
Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Trp Asp Ile Glu
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cca cag aat att gca cta aca aac ggc agc cag agc gcg ttt ttc tac     336
Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr
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tta ttt aat ctg ttt gcc gga cgc cgt gcc gat ggt cgg gtt aaa aaa     384
Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys
        115                 120                 125

gtg ctg ttc ccg ctt gca ccg caa tat att ggc tat gct gat gcc gga     432
Val Leu Phe Pro Leu Ala Pro Gln Tyr Ile Gly Tyr Ala Asp Ala Gly
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ccg gaa ggc cag ttt aaa tac cac gtc gat ttt gag cat ctg cat att      528
Pro Glu Gly Gln Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile
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ggc gaa gaa acc ggg atg att tgc gtc tcc cgg ccg acg aat cca aca      576
Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr
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ggc aat gtg att act gac gaa gag ttg ctg aag ctt gac gcg ctg ggc      624
Gly Asn Val Ile Thr Asp Glu Glu Leu Leu Lys Leu Asp Ala Leu Gly
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aat caa cac ggc att ccg ctg gtg att gat aac gct tat ggc gtc ccg      672
Asn Gln His Gly Ile Pro Leu Val Ile Asp Asn Ala Tyr Gly Val Pro
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Phe Pro Gly Ile Ile Phe Ser Glu Ala Arg Pro Leu Trp Asn Pro Asn
225                 230                 235                 240

atc gtg ctg tgc atg agt ctt tcc aag ctg ggt cta cct ggc tcc cgc      768
Ile Val Leu Cys Met Ser Leu Ser Lys Leu Gly Leu Pro Gly Ser Arg
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tgc ggc att atc atc gcc aat gaa aaa atc atc acc gcc atc acc aat      816
Cys Gly Ile Ile Ile Ala Asn Glu Lys Ile Ile Thr Ala Ile Thr Asn
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atg aac ggc att atc agc ctg gca cct ggc ggt att ggt ccg gcg atg      864
Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met
        275                 280                 285

atg tgt gaa atg att aag cgt aac gat ctg ctg cgc ctg tct gaa aca      912
Met Cys Glu Met Ile Lys Arg Asn Asp Leu Leu Arg Leu Ser Glu Thr
    290                 295                 300

gtc att aaa ccg ttt tac tac cag cgt gtt cag gaa act atc gcc atc      960
Val Ile Lys Pro Phe Tyr Tyr Gln Arg Val Gln Glu Thr Ile Ala Ile
305                 310                 315                 320

att cgc cgc tat tta ccg gaa aat cgc tgc ctg att cat aaa ccg gaa      1008
Ile Arg Arg Tyr Leu Pro Glu Asn Arg Cys Leu Ile His Lys Pro Glu
                325                 330                 335

gga gcc att ttc ctc tgg cta tgg ttt aag gat ttg ccc att acg acc      1056
Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr
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aaa cag ctc tat cag cgc ctg aaa gca cgc ggc gtg ctg atg gtg ccg      1104
Lys Gln Leu Tyr Gln Arg Leu Lys Ala Arg Gly Val Leu Met Val Pro
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Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His
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Ile Met Leu Gly Gly Gly Asn Pro Ala Gln Ile Pro Glu Met Gln Asp
        35                  40                  45

Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr
    50                  55                  60

Asp Ala Leu Cys Asn Tyr Asp Gly Pro Gln Gly Lys Thr Glu Leu Leu
 65                  70                  75                  80

Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Trp Asp Ile Glu
                 85                  90                  95

Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr
            100                 105                 110

Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys
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Val Leu Phe Pro Leu Ala Pro Glu Tyr Ile Gly Tyr Ala Asp Ala Gly
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Leu Glu Glu Asp Leu Phe Val Ser Ala Arg Pro Asn Ile Glu Leu Leu
145                 150                 155                 160

Pro Glu Gly Gln Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile
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Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr
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Gly Asn Val Ile Thr Asp Glu Glu Leu Leu Lys Leu Asp Ala Leu Gly
        195                 200                 205

Asn Gln His Gly Ile Pro Leu Val Ile Asp Asn Ala Tyr Gly Val Pro
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Phe Pro Gly Ile Ile Phe Ser Glu Ala Arg Pro Leu Trp Asn Pro Asn
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Cys Gly Ile Ile Ile Ala Asn Glu Lys Ile Ile Thr Ala Ile Thr Asn
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Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met
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Met Cys Glu Met Ile Lys Arg Asn Asp Leu Leu Arg Leu Ser Glu Thr
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Val Ile Lys Pro Phe Tyr Tyr Gln Arg Val Gln Glu Thr Ile Ala Ile
305                 310                 315                 320

Ile Arg Arg Tyr Leu Pro Glu Asn Arg Cys Leu Ile His Lys Pro Glu
                325                 330                 335

Gly Ala Ile Phe Leu Trp Leu Trp Phe Lys Asp Leu Pro Ile Thr Thr
            340                 345                 350

Lys Gln Leu Tyr Gln Arg Leu Lys Ala Arg Gly Val Leu Met Val Pro
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Gly His Asn Phe Phe Pro Gly Leu Asp Lys Pro Trp Pro His Thr His
    370                 375                 380

Gln Cys Met Arg Met Asn Tyr Val Pro Glu Pro Glu Lys Ile Glu Ala
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Gly Val Lys Ile Leu Ala Glu Glu Ile Glu Arg Ala Trp Ala Glu Ser
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His


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Ile Tyr Asn Asp Thr Lys Leu Thr Ala Glu Trp Arg Leu Ser Thr Asp
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Val Leu Arg Ser Ala Asp Glu Tyr Gly Ile Gln Val Met Asn Leu Phe
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Gln Gln Asp Lys Leu Asp Pro Thr Leu Val Glu Gly Val Ile Ile Ser
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Ser Val Val Pro Asn Ile Met Tyr Ser Leu Glu His Met Ile Arg Lys
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Tyr Phe Lys Ile Asn Pro Leu Val Val Gly Pro Gly Ile Lys Thr Gly
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Arg Arg Thr Ala Asp Glu Tyr Phe Val Trp Leu Asn Thr Leu Met Gln
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Leu Lys Gly Leu Gln Gly Arg Ile Ser Glu Ala Ile Ile Ser Ser Thr
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Ala Pro Arg Val Val Phe Asn Leu Arg Val Leu Cys Asn Arg Tyr Phe
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Ala Pro Arg Val Asp Pro Gly Thr Thr Val Gly Pro Asp Arg Leu Val
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ctgggtgagc aaaaacagga aggcaaaatg ccgcaaaaaa gggaataagg gcgacacgga 10200

aatgttgaat actcatactc ttcctttttc aatattattg aagcatttat cagggttatt 10260

gtctcatgag cggatacata tttgaatgta tttagaaaaa taaacaaata ggggttccgc 10320

gcacatttcc ccgaaaagtg ccacctgacg tctaagaaac cattattatc atgacattaa 10380

cctataaaaa taggcgtatc acgaggccct ttcgtcttca agaatt 10406

<210> 83
<211> 4191
<212> DNA
<213> Artificial Sequence

<220>
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pAN163 plasmid

<400> 83
[illegible] 60

[illegible] 120

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atcggcgatc ctcaagccat tcctgctatg atcaagtcat taagcgactc cagcaagctt 300

gttcgctggc gtgccgccat gttcctgtac gaagtcggcg atgaaagtgc aattgaagct 360

ttgcggcctg ccgaagatga ccccgaattt gaggtcagcc ttcaagtcaa aatggcgctt 420

gaacgtattg agcatggaga agaagcaaaa ggttctgttt ggaacaaaat gacggaaagc 480

agaaaaaaag gcgaataaag ataaaaaagg tgcagatcat gcaccttttt tatgtgaatt 540

ggtcgaccga aacagcagtt ataaggcatg aagctgtccg gtttttgcaa aagtggctgt 600

gactgtaaaa agaaatcgaa aaagaccgtt ttgtgtgaaa acggtctttt tgtttccttt 660

taaccaactg ccataactcg aggcctacct agcttccaag aaagatatcc taacagcaca 720

agagcggaaa gatgttttgt tctacatcca gaacaacctc tgctaaaatt cctgaaaaat 780

tttgcaaaaa gttgttgact ttatctacaa ggtgtggtat aataatctta acaacagcag 840

gacgctctag aggaggagac accatggcag aattacgcag taatatgatc acacaaggaa 900

tcgatagagc tccgcaccgc agtttgcttc gtgcagcagg ggtaaaagaa gaggatttcg 960

gcaagccgtt tattgcggtg tgtaattcat acattgatat cgttcccggt catgttcact 1020

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caatgcgcat caacattccg acgatttttg tcagcggcgg accgatggcg gcaggaagaa 1320

caagttaccg gcgaaaaatc tccctttcct cagtattcga aggggtaggc gcctaccaag 1380

cagggaaaat caacgaaaac gagcttcaag aactagagca gttcggatgc ccaacgtgcg 1440

gctcttgctc aggcatgttt acggcgaact caatgaactg tctgtcagaa gcacttagtc 1500

ttgcttggcc aggtaatgga accattctgg caacatctcc ggaacgcaaa gagtttgtga 1560

gaaaatcggc tgcgcaatta atggaaacga tttgcaaaaa tatcaaaccg cgtgatattg 1620

ttacactaaa atcgattgat aacgcgtttg cactcaatat ggcggtcgga actctacaaa 1680

[illegible]

[illegible]

[illegible]

[illegible]
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ctcaggacga ggcgcttgac ggcattatca accgaaaagt aaaagaaggc gacgttgtca 2160
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cccaaatcgt tggaatggga ctcgggccaa aagtggcatt gattacggac ggacgttttt 2280
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cgaaagtgaa aaccggctac ctggcacgtt attctaaact tgtgacaagt gccaacaccg 2520
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[illegible]
[illegible]
[illegible]
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cggattgaac ggggggttcg tgcatacagt ccagcttgga gcgaactgcc tacccggaac 3960

tgagtgtcag gcgtggaatg agacaaacgc ggccataaca gcggaatgac accggtaaac 4020

cgaaaggcag gaacaggaga gcgcacgagg gagccgccag ggaaacgcc tggtatcttt 4080

atagtcctgt cgggtttcgc caccactgat ttgagcgtca gatttcgtga tgcttgtcag 4140

gggggcggag cctatggaaa aacggctttg ccgcggccct ctcatttccc t 4191

<210> 84
<211> 702
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(699)

<400> 84
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Met Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
1 5 10 15

tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
20 25 30

cat aaa aca gaa gat gag ttt ggg atg att ttg cgc tcc tta ttt gat 144
His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
35 40 45

cat tcc ggg ctt atg ttt gaa cag att gat ggc att att att tcg tca 192
His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
50 55 60

gta gtg ccg cca atc atg ttt gcg tta gaa aga atg tgc aca aaa tac 240
Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65 70 75 80

ttt cat atc gaa cct caa att gtt ggt cca ggt atg aaa acc ggt tta 288
Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
85 90 95

aat ata aaa tat gat aat ccg aaa gaa gta ggg gca gac aga atc gta 336
Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
100 105 110

[illegible] 384
Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
115 120 125

[illegible] 432
Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
130 135 140

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tac atg ggc ggg gcg att gcc cct ggg att aca att tcg aca gag gcg      480
Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145                 150                 155                 160

ctt tac tcg cgt gca gca aag ctt cct cgt atc gaa atc acc cgg ccc      528
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
                165                 170                 175

gac aat att atc gga aaa aac act gtt agc gcg atg caa tct gga att      576
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
            180                 185                 190

tta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag cga atg aaa      624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
        195                 200                 205

tgg cag gca aaa cag gac cca agg tca ttg cga cag gag gcc tgg cgc      672
Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
    210                 215                 220

cgc tca ttg cga acg aat cag att gta tag                              702
Arg Ser Leu Arg Thr Asn Gln Ile Val
225                 230


<210> 55
<211> 233
<212> PRT
<213> Bacillus subtilis

<400> 55
Met Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1              5                   10                  15

Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
            20                  25                  30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
        35                  40                  45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
    50                  55                  60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
65                  70                  75                  80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
                85                  90                  95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
            100                 105                 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
        115                 120                 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Gln Asn Lys Gln
    130                 135                 140

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
145                 150                 155                 160
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Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
                165                 170                 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
            180                 185                 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
        195                 200                 205

Trp Gln Ala Lys Gln Asp Pro Arg Ser Leu Arg Gln Glu Ala Trp Arg
    210                 215                 220

Arg Ser Leu Arg Thr Asn Gln Ile Val
225                 230

<210> 86
<211> 1623
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (1)..(1620)

<400> 86
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Met Tyr Leu Ala Phe Gln Val Gln Lys Leu Met Arg Tyr Leu Thr Leu
1               5                   10                  15

tac aag ata aag gac ctg aaa tta tcg ttg ccc ggc acg aac aaa acg      96
Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
            20                  25                  30

cag caa ttc atg gct caa gca gtc ggt cgt tta act gga aaa ccg gga     144
Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly
        35                  40                  45

gtc gtg tta gtc aca tca gga ccg ggt gcc tct aac ttg gca aca ggc     192
Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly
    50                  55                  60

ctg ctg aca gcg aac act gaa gga gac cct gtc gtt gcg ctt gct gga     240
Leu Leu Thr Ala Asn Thr Glu Gly Asp Pro Val Val Ala Leu Ala Gly
65                  70                  75                  80

aac gtg att cgt gca tat cgt tta aaa cgg aca cat caa tct ttg gat     288
Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
                85                  90                  95

aat gcg gct tta ttc caa ccg att aca aaa tac agt gta gaa gtt caa     336
Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Glu Val Gln
            100                 105                 110

gat gta aaa aat ata cct gaa gct gtt aca aat gct ttt cgt att gct     384
Asp Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Phe Arg Ile Ala
        115                 120                 125

[illegible]                                                         432
Ser Ala Gly Gln Ala Gly Ala Ala Phe Val Ser Phe Ile Gln Asp Val
    130                 135                 140
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gtg aat gaa gtc aca aat acg aaa aac gtg cgt gct gtt gca gcg cca     480
Val Asn Glu Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro
145                 150                 155                 160

aaa ctc ggt cct gca gca gat gat gca atc agt gcg gct ata gca aaa     528
Lys Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys
                165                 170                 175

atc caa aca gca aaa ctt cct gtc gtt ttg gtc ggc atg aaa ggc gga     576
Ile Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly
            180                 185                 190

aga ccg gaa gca att aaa gcg gtt cgc aag ctt ttg aaa aag gtt cag     624
Arg Pro Glu Ala Ile Lys Ala Val Arg Lys Leu Leu Lys Lys Val Gln
        195                 200                 205

ctt cca ttt gtt gaa aca tat caa gct gct ggt act ctt tct aga gat     672
Leu Pro Phe Val Glu Thr Tyr Gln Ala Ala Gly Thr Leu Ser Arg Asp
    210                 215                 220

tta gag gat caa tat ttt ggc cgt atc ggt ttg ttc cgc aac cag cct     720
Leu Glu Asp Gln Tyr Phe Gly Arg Ile Gly Leu Phe Arg Asn Gln Pro
225                 230                 235                 240

ggc gat tta ctg cta gag cag gca gat gtt gtt ctg acg atc ggc tat     768
Gly Asp Leu Leu Leu Glu Gln Ala Asp Val Val Leu Thr Ile Gly Tyr
                245                 250                 255

gac ccg att gaa tat gat ccg aaa ttc tgg aat atc aat gga gac cgg     816
Asp Pro Ile Glu Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg
            260                 265                 270

aca att att cat tta gac gag att att gct gat att gat cat gct tac     864
Thr Ile Ile His Leu Asp Glu Ile Ile Ala Asp Ile Asp His Ala Tyr
        275                 280                 285

caa cct gat ctt gaa ttg atc ggt gac att ccg tcc acg atc aat cat     912
Gln Pro Asp Leu Glu Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His
    290                 295                 300

atc gaa cac gat gct gtg aaa gtg gaa ttt gca gag cgt gag cag aaa     960
Ile Glu His Asp Ala Val Lys Val Glu Phe Ala Glu Arg Glu Gln Lys
305                 310                 315                 320

atc ctt tct gat tta aaa caa tat atg cat gaa ggt gag cag gtg cct    1008
Ile Leu Ser Asp Leu Lys Gln Tyr Met His Glu Gly Glu Gln Val Pro
                325                 330                 335

gca gat tgg aaa tca gac aga gcg cac cct ctt gaa atc gtt aaa gag    1056
Ala Asp Trp Lys Ser Asp Arg Ala His Pro Leu Glu Ile Val Lys Glu
            340                 345                 350

ttg cgt aat gca gtc gat gat cat gtt aca gta act tat gat att ggt    1104
Leu Arg Asn Ala Val Asp Asp His Val Thr Val Thr Tyr Asp Ile Gly
        355                 360                 365

tcg cat tcc att tgg atg tca cgt tat ttc cgt agc tat gaa cct tta    1152
Ser His Ser Ile Trp Met Ser Arg Tyr Phe Arg Ser Tyr Glu Pro Leu
    370                 375                 380
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aca tta atg atc agt aac ggt atg caa aca ctc ggc gtt gcg ctt cct 1200
Thr Leu Met Ile Ser Asn Gly Met Gln Thr Leu Gly Val Ala Leu Pro
385 390 395 400

tgg gca atc ggc gct tca ttg gtg aaa ccg gga gaa aaa gtg gtt tct 1248
Trp Ala Ile Gly Ala Ser Leu Val Lys Pro Gly Glu Lys Val Val Ser
405 410 415

gtc tct ggt gac ggc ggt ttc tta ttc tca gca atg gaa tta gag aca 1296
Val Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr
420 425 430

gca gtt cga cta aaa gca cca att gta cac att gta tgg aac gac agc 1344
Ala Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser
435 440 445

aca tat gac atg gtg cat ttc cag caa ttg aaa aaa tat aac cgt aca 1392
Thr Tyr Asp Met Val His Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr
450 455 460

tct gcg gtc gat ttc gga aat atc gat atc gtg aaa tat gcg gaa agc 1440
Ser Ala Val Asp Phe Gly Asn Ile Asp Ile Val Lys Tyr Ala Glu Ser
465 470 475 480

ttc gga gca act gcg ttg cgc gta gaa tca cca gac cag ctg gca gat 1488
Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
485 490 495

gtt ctg cgt caa ggc atg aac gct gaa ggt cct gtc atc atc gat gtc 1536
Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val
500 505 510

ccg gtt gat tac agt gat aac att aat tta gca agt gat aaa ctt ccg 1584
Pro Val Asp Tyr Ser Asp Asn Ile Asn Leu Ala Ser Asp Lys Leu Pro
515 520 525

aaa gaa ttc ggg gaa ctc atg aaa acg aaa gct ctc tag 1623
Lys Glu Phe Gly Glu Leu Met Lys Thr Lys Ala Leu
530 535 540

<210> 87
<211> 540
<212> PRT
<213> Bacillus subtilis

<400> 87
Met Tyr Leu Ala Phe Gln Val Gln Lys Leu Met Arg Tyr Leu Thr Leu
1 5 10 15

Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
20 25 30

Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly
35 40 45

Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly
50 55 60

Leu Ile Thr Ala Asn Thr Gln Gly Arg Pro Val Val Ala Leu Ala Gly
65 70 75 80

```
Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
                85                  90                  95

Asn Ala Ala Leu Phe Gln Pro Ile Thr Lys Tyr Ser Val Glu Val Gln
            100                 105                 110

Asp Val Lys Asn Ile Pro Glu Ala Val Thr Asn Ala Phe Arg Ile Ala
        115                 120                 125

Ser Ala Gly Gln Ala Gly Ala Ala Phe Val Ser Phe Pro Gln Asp Val
    130                 135                 140

Val Asn Glu Val Thr Asn Thr Lys Asn Val Arg Ala Val Ala Ala Pro
145                 150                 155                 160

Lys Leu Gly Pro Ala Ala Asp Asp Ala Ile Ser Ala Ala Ile Ala Lys
                165                 170                 175

Ile Gln Thr Ala Lys Leu Pro Val Val Leu Val Gly Met Lys Gly Gly
            180                 185                 190

Arg Pro Glu Ala Ile Lys Ala Val Arg Lys Leu Leu Lys Lys Val Gln
        195                 200                 205

Leu Pro Phe Val Glu Thr Tyr Gln Ala Ala Gly Thr Leu Ser Arg Asp
    210                 215                 220

Leu Glu Asp Gln Tyr Phe Gly Arg Ile Gly Leu Phe Arg Asn Gln Pro
225                 230                 235                 240

Gly Asp Leu Leu Leu Glu Gln Ala Asp Val Val Leu Thr Ile Gly Tyr
                245                 250                 255

Asp Pro Ile Glu Tyr Asp Pro Lys His Trp Asn Ile Asn Gly Asp Arg
            260                 265                 270

Thr Ile Ile His Leu Asp Glu Ile Ile Ala Asp Ile Asp His Ala Tyr
        275                 280                 285

Gln Pro Asp Leu Glu Leu Ile Gly Asp Ile Pro Ser Thr Ile Asn His
    290                 295                 300

Ile Glu His Asp Ala Val Lys Val Glu Phe Ala Glu Arg Glu Gln Lys
305                 310                 315                 320

Ile Leu Ser Asp Leu Lys Gln Tyr Met His Glu Gly Glu Gln Val Pro
                325                 330                 335

Ala Asp Trp Lys Ser Asp Arg Ala His Pro Leu Glu Ile Val Lys Glu
            340                 345                 350

Leu Arg Asn Ala Val Asp Asp His Val Thr Val Thr Cys Asp Ile Gly
        355                 360                 365

Ser His Ser Ile Trp Met Ser Arg Tyr Phe Arg Ser Tyr Glu Pro Leu
    370                 375                 380

Thr Leu Met Ile Ser Asn Gly Met Gln Thr Leu Gly Val Ala Leu Pro
385                 390                 395                 400
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Trp Ala Ile Gly Ala Ser Leu Val Lys Pro Gly Glu Lys Val Val Ser
                405                 410                 415

Val Ser Gly Asp Gly Gly Phe Leu Phe Ser Ala Met Glu Leu Glu Thr
            420                 425                 430

Ala Val Arg Leu Lys Ala Pro Ile Val His Ile Val Trp Asn Asp Ser
        435                 440                 445

Thr Tyr Asp Met Val His Phe Gln Gln Leu Lys Lys Tyr Asn Arg Thr
    450                 455                 460

Ser Ala Val Asp Phe Gly Asn Ile Asp Ile Val Lys Tyr Ala Glu Ser
465                 470                 475                 480

Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
                485                 490                 495

Val Leu Arg Gln Gly Met Asn Ala Glu Gly Pro Val Ile Ile Asp Val
            500                 505                 510

Pro Val Asp Tyr Ser Asp Asn Ile Asn Leu Ala Ser Asp Lys Leu Pro
        515                 520                 525

Lys Glu Phe Gly Glu Leu Met Lys Thr Lys Ala Leu
    530                 535                 540


<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ribosome
      binding site

<220>
<221> misc_feature
<222> (14)..(20)
<223> n = a, c, g, or t

<400> 48
agaaaggagg taannnnnnn atg                                          23


<210> 49
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: [illegible]
      C terminus

<400> 49
Ile Arg Glu Met Glu Arg Ile
  1               5


<210> 50
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<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PanC
      C terminus

<400> 90
Ile Arg Glu Arg Arg
  1               5


<210> 91
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PanC
      C terminus

<400> 91
Ile Arg Arg Lys Glu Val Asn
  1               5

<210> 92
<211> 6655
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Recombinant
      pAN33c plasmid

<400> 92
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tcggtgcggg cctcttcgct attacgccag ctggcgaaag ggggatgtgc tgcaaggcga 120

ttaagttggg taacgccagg gttttcccag tcacgacgtt gtaaaacgac ggccagtgaa 180

ttgtaatacg actcactata gggcgaattg ggcccgacgt cgcatgcacc aggcttctca 240

[illegible] tagaaaacct cttgaatgaa [illegible] 300

[illegible] 360

aagaagagcc gcgttatctc caagaaagaa [illegible] 420

[illegible] 480

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]
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gatcaaatcg cttacgaaat tgatcaggaa attcagcgca tcatcaaaga atgttatgag 840
cgtgcgaaac aaatcctgac tgaaaatcgt gacaagcttg aattgattgc ccaaacgctt 900
ctgaaagttg aaacgcttga cgctgaacaa atcaaacacc ttatcgatca tggaacatta 960
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ccggctgacg ctggcagttt ttttatgtaa atgattggct cagctcgggc ttttacaatc 1140
atccaattct ggtatcgatt tgtttacaaa tgagccgctg atcgtgtatg gtattgtaga 1200
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